OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: April 24, 2005, 05:43:39 ; Search time 201 Seconds
(without alignments)
2165.421 Million cell updates/sec

Title: 1377
Perfect score: 1377
Sequence: 1 MMKTLSSGNCTLSVPAKNSY.........IKAKVLREGQARERDKCTIQ 266

Searched: US-09-778-963B-2

Scoring table: BLOSUM62
Xgapop 10.0 ; Xgapext 0.5
Ygapop 10.0 ; Ygapext 0.5
Fgapop 6.0 ; Fgapext 7.0
Delop 6.0 ; Delext 7.0

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters:
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-DB=Issued_Patents NA -QFMT=fastap -SUFFIX=rnl -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Issued_Patents NA:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1372	99.6	837	4	US-09-709-103-40	Sequence 40, Appl
2	1372	99.6	837	4	US-09-439-410A-40	Sequence 40, Appl
3	1372	99.6	837	4	US-09-439-410A-73	Sequence 73, Appl
4	911	66.2	9259	4	US-09-949-016-5022	Sequence 5022, Ap
5	879	63.8	846	4	US-09-709-016-16764	Sequence 16764, A
6	879	63.8	846	4	US-09-709-103-1	Sequence 1, Appli
7	879	63.8	846	4	US-09-439-410A-1	Sequence 1, Appli
8	879	63.8	1740	4	US-09-709-103-45	Sequence 45, Appl
9	879	63.8	1740	4	US-09-439-410A-45	Sequence 45, Appl
10	879	63.8	1801	4	US-09-709-103-3	Sequence 3, Appli
11	879	63.8	1841	3	US-09-439-410A-3	Sequence 3, Appli
12	876.5	63.7	1689	3	US-09-053-374A-4	Sequence 4, Appli
13	820	59.5	3079	3	US-09-053-374A-6	Sequence 6, Appli
14	817	59.3	3986	2	US-09-053-374A-3	Sequence 3, Appl
15	817	59.3	4990	4	US-09-439-410A-73	Sequence 73, Appl
16	344	25.0	1108	4	US-09-620-312D-945	Sequence 945, App
17	298	21.6	432	2	US-09-621-976-17745	Sequence 17745, A
18	294.5	21.4	3300	4	US-09-620-312D-456	Sequence 456, App
19	285	20.7	615	1	US-09-247-196A-5	Sequence 5, Appl
20	285	20.7	615	5	PCT-US95-06420-5	Sequence 5, Appl
21	280.5	20.4	551	5	US-09-755-298A-25	Sequence 25, Appl
22	280.5	20.4	567	1	US-09-223-588-1	Sequence 1, Appli
23	280.5	20.4	570	1	US-09-167-322-12	Sequence 12, Appl
24	280.5	20.4	4480	3	US-08-884-866A-11	Sequence 11, Appl
25	279.5	20.3	570	3	US-08-306-691B-15	Sequence 15, Appl
26	279.5	20.3	567	3	US-09-023-655-1145	Sequence 1145, App
27	279.5	20.3	5775	4	US-09-949-016-702	Sequence 702, App
28	279.5	20.3	5775	5	PCT-US93-06251-29	Sequence 29, Appli
29	279.5	20.3	5775	2	US-09-223-588-2	Sequence 2, Appli
30	278.5	20.2	567	4	US-09-949-016-4767	Sequence 4767, Ap
31	278.5	20.2	1368	4	US-08-884-866A-9	Sequence 9, Appli
32	278.5	20.2	480	3	US-09-755-298A-27	Sequence 27, Appl
33	277.5	20.2	570	4	US-08-429-964-85	Sequence 85, Appl
34	277.5	20.2	607	2	US-08-429-796A-5513	Sequence 5513, Ap
35	274.5	19.9	711	5	US-08-248-796A-85	Sequence 16, Appl
36	274	19.9	2436	1	US-08-306-691B-16	Sequence 16, Appl
37	274	19.9	2436	4	US-09-963-137-161	Sequence 161, Appl
38	274	19.9	2436	4	US-09-963-137-165	Sequence 165, App
39	273.5	19.9	574	2	US-08-429-964-83	Sequence 83, Appl
40	269.5	19.6	798	4	US-09-248-796A-5510	Sequence 5510, A
41	269.5	19.6	3026	4	US-09-963-137-136	Sequence 136, App
42	269.5	19.6	3026	4	US-09-963-137-140	Sequence 140, App
43	255.5	18.6	450	3	US-08-884-866A-10	Sequence 10, Appl
44	245.5	17.8	523	4	US-09-270-767-25712	Sequence 25712, A
45	245.5	17.8	600	4	US-09-270-767-10334	Sequence 10334, A

ALIGNMENTS

RESULT 1
US-09-709-103-40
; Sequence 40, Application US/09709103
; Patent No. 6733991
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/709,103
; CURRENT FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 40
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(834)
; OTHER INFORMATION:
US-09-709-103-40

Alignment Scores:
Pred. No.:   3.49e-180
Score: 1372.00
Percent Similarity: 99.62%
Best Local Similarity: 99.64%
Query Match: 4

Length: 837
Matches: 265
Conservative: 0
Mismatches: 1
Indels: 0
Gaps: 0

US-09-778-963B-2 (1-266) x US-09-709-103-40 (1-837)

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Qy   1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  37 ATGATGAAGACTTTGTCCAGCGGGAACTGCACGCTCAGTGTGCCGGCCAAAAACTCATAC 96
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; OTHER INFORMATION:
; US-09-433-410A-40

Alignment Scores:
Pred. No.:
; Patent No. 6746852
; Sequence 40, Application US/09439410A

GENERAL INFORMATION:
APPLICANT: Cismowski, Mary
APPLICANT: Duzic, Emir
TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: 1919/60388-B
CURRENT APPLICATION NUMBER: US/09/439,410A
CURRENT FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1

SEQ ID NO 40
LENGTH: 837
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(834)

RESULT 2
US-09-439-410A-40
Sequence 40, Application US/09439410A
Patent No. 6746852

	Length:	837
Score:	3.49e-180	Matches:	265
Percent Similarity:	1372.00	Conservative:	0
Best Local Similarity:	99.62%	Mismatches:	1
Query Match:	99.62%	Indels:	0
DB:	99.64%	Gaps:	0
	4		

US-09-778-963B-2 (1-266) x US-09-439-410A-40 (1-837)

Qy	1	MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr	20
Db	37	ATGATGAAGACHTTGTCCAGCGGGGGAACGTGCACGCTCAGTGTGCCCGCAAAAAACTCATAC	96

| Qy | 21 | ArgMetValValLeuGlyAlaSerArgArgValGlyLysSerSerIleValSerArgPheLeu | 40 |
| Db | 97 | CGCATGGTGGTTCTGGGTGCTTCGGGGTGGGCCAAGAGCTCCATCGTGTCTCGGTTCCTC | 156 |

| Qy | 41 | AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr | 60 |
| Db | 157 | AATGGGCGCTTTGAGGACCAGTACACACCCACCATCGAGGACTTCCACCGTAAGGTATAC | 216 |

| Qy | 61 | AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe | 80 |
| Db | 217 | AACATCCGCGGCGACATGTACCAGCTCGACATCCTGGACACCTCTGGCAACCACCCCTTC | 276 |

| Qy | 81 | ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPhelleLeuValPheSerLeu | 100 |
| Db | 277 | CCCGCCATGCGCAGGCTGTCCATCCTCACGGGGGATGTCTTCATCCTGGTGTTCAGCCTG | 336 |

| Qy | 101 | AspAsnArgGluSerPheAspGluValAlaArgLeuGlnIleLeueuGluValLys | 120 |
| Db | 337 | GATAACCGGGAGTCCTTCGATGAGGTCGCAAGGCTCCAGATCTTAGAAGTCAAGCTCAAG | 396 |

| Qy | 121 | SerCysLeuLysAsnLysThrLysGluAlaAlaGluLeuProMetValIleLeuGlyAsn | 140 |
| Db | 397 | TCCTGCCTGAAGAACAAGACCAAGGAGGCGGCAGAGCTGCCCATGGTCATCCTGGGCAAC | 456 |

| Qy | 141 | LysAsnAspHisGlyLysGlnLeuCysArgGlnValProThrThrGluAlaGluLeuVal | 160 |
| Db | 457 | AAGAACGACCACGGGCAGTTGTGCCGCCAAGTGCCCACCACGGAGGCTGAGCTGGTG | 516 |

| Qy | 161 | SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaLysAsnThrAsnValAsp | 180 |
| Db | 517 | TCGGGCGACGAGAACTCGGCCTACTTCGAGGTGTCGGCCAAGAACACCAACGTGGAC | 576 |

| Qy | 181 | GluMetPheTyrValLeuPheSerMetAlaLysLeuProHisGluMetSerProAlaLeu | 200 |
| Db | 577 | GAGATGTTCTACGTGCTCTTCAGCATGGCCAAGCTGCCACACGAGATGAGCCCCGCCCTG | 636 |

| Qy | 201 | HisArgLysIleSerValGlnIleTyrGlyAspAlaPheHisIleProArgProPheSerVal | 220 |
| Db | 637 | CATCGCAAGATCTCCGTGCAGATCTACGGTGACGCCTTCCACCCCAGGCCCTTCTGCATGGC | 696 |

| Qy | 221 | ArgValLysGluMetAspAlaTyrGlyMetValSerProPheAlaArgArgProSerVal | 240 |
| Db | 697 | CGCGTCAAGGAGATGGACGCCTATGGCATGGTCTCGCCCTTCGCCCGCCGCCCCAGCGTC | 756 |

| Qy | 241 | AsnSerAspLeuLysSerTyrIleLeuLysAlaValLeuArgGluLysGlnAlaArgGluArg | 260 |
| Db | 757 | AACAGTGACCTCAAGTCATACATCAAGGCCGTCCTTCGGGAAAGGCCAGGCCCGTGAGAGG | 816 |

| Qy | 261 | AspLysCysThrIleGln | 266 |
| Db | 817 | GACAAGTGCACCATCCAG | 834 |

RESULT 3
US-09-949-016-5022
; Sequence 5022, Application US/09949016
; Patent No. 6812339

; RESULT 2
; US-09-439-410A-40

GENERAL INFORMATION:
APPLICANT: VENTER,
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5022
LENGTH: 837
TYPE: DNA
ORGANISM: Human
US-09-949-016-5022

Alignment Scores:
Pred. No.:
Score: 3.49e-180　　　Length: 837
Matches: 1372.00　　　Matches: 265
Percent Similarity: 99.62%　Conservative: 1
Best Local Similarity: 99.62%　Mismatches: 1
Query Match: 99.64%　Indels: 0
DB:　　　Gaps: 0

US-09-778-963B-2 (1-266) x US-09-949-016-5022 (1-837)

Qy　　1　MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr　20
Db　37　ATGATGAAGACTTTGTCCAGCGGGAACTGCACGCTCAGTGTGCCCCCAAAAAACTCATAC　96

Qy　21　ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu　40
Db　97　CGCATGGTGGTGCTCGGGGCGTCGCGGGTGGGCAAGAGCTCCATCGTGTCTCGCTTCCTC　156

Qy　41　AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr　60
Db　157　AATGGCCGCTTTGAGGACCAGTACACACCCACCATCGAGGACTTTCACCGTAAGGTATAC　216

Qy　61　AsnIleArgGlyAspMetTyrGlnIleLeuAspIleLeuAspThrSerGlyAsnHisProPhe　80
Db　217　AACATCCGCGGCGACATGTACCAGATCCTGGATACCTCTGGGCAACCACCCCTTC　276

Qy　81　ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu　100
Db　277　CCCGCCATGCGCAGGCTGTCCATCCTCACAGGGGATGTCTTCATCCTGGTGTTCAGCCTG　336

Qy　101　AspAsnArgGluSerPheAspGluValLysArgLeuGlnLysGlnIleLeuGluValLys　120
Db　337　GATAACCGGGAGTCCTTCGATGAGGTCAAGCGCCTTCAGAAGCAGATCCTGGAGGTCAAG　396

Qy　121　SerCysGluLeuAsnLysThrLysGlnAlaAlaGluLeuProMetValIleCysGlyAsn　140
Db　397　TCCTGCGCCTGAAGAACAAGACAAAGCAAGCGGCGGACTGGCCCCATGGTCATCTGTGGCAAC　456

Qy　141　LysAsnAspHisGlyLysLeuLysGlnValProThrThrGlyAlaGluLeuLeuVal　160
Db　457　AAGAACGACCGGAAGCTGTGCCCACCACCGGCCGAGCTGTTGGTG　516

Qy　161　SerGlyAspAspLeuSerPheAlaTyrPheGluValSerAlaLysAspSerThrAsnValAsp　180
Db　517　TCGGGCGACGAGAACTGCGCCTACTTCGAGGTGTCGGCCAAGAAGAACACCAACGTGGAC　576

Qy　181　GluMetPheTyrValLeuPheSerMetAlaLysLeuProHisGluMetSerProAlaLeu　200
Db　577　GAGATGTTCTACGTGCTCTTCAGCATGGCCAAGCTGCCACACGAGATGAGCCCCGCCCTG　636

Qy　201　HisArgLysIleSerValGlnThrTyrGlyAspAlaPheHisProArgProPheCysMetArg　220
Db　637　CATCGCAAAGATCTCCGTGCAGACGTACGGTGACGCCTTCCACCCCAGGCCGCCTTCTGCATGCGC　696

Qy　221　ArgValLysGluGlnMetAspAlaTyrGlyMetValSerProPheAlaArgArgProSerVal　240
Db　697　CGCGTCAAGGAGCAGATGGACGCCTATGGCATGGTCTCGCCCTTCGCCCGCCGCCCAGCCGTC　756

Qy　241　AsnSerPheAspLeuLysTyrIleLysValValLeuArgGluGluGlnAlaArgGlyArg　260
Db　757　AACAGTGACCTCAAGTACATCAAGGCGCCAAGGGTCCTTCGGGAAGGCCAGCCGCCTGAGAGG　816

Qy　261　ArgLysCysThrIleGln　266
Db　817　GACAAGTGCACCATCCAG　834

RESULT 4
US-09-949-016-16764
Sequence 16764, Application US/09949016
Patent No. 6812339
SEQ ID NO 16764
LENGTH: 9259
TYPE: DNA
ORGANISM: Human
US-09-949-016-16764

GENERAL INFORMATION:
APPLICANT: VENTER,
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16764
LENGTH: 9259
TYPE: DNA
ORGANISM: Human
US-09-949-016-16764

Alignment Scores:
Pred. No.:
Score: 1.73e-114　　　Length: 9259
Matches: 911.00　　　Matches: 176
Percent Similarity: 98.33%　Conservative: 1
Best Local Similarity: 97.78%　Mismatches: 3
Query Match: 66.16%　Indels: 0
DB:　　　Gaps: 0

US-09-778-963B-2 (1-266) x US-09-949-016-16764 (1-9259)

Qy　87　SerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgGluSerPhe　106
Db　6717　TCTCTCCCTGCAGGGGATGTCTTCATCCTGGTGTTCAGCCTGGATAACCGGGAGTCCTTC　6776

Qy　107　AspGluValLysArgLeuGlnLysGlnIleLeuGluValLysSerCysGluLeuAsnLys　126
Db　6777　GATGAGGTCAAGCGCCTTCAGAAGCAGATCCTGGAGGTCAAGTCCTGCGCCCTGAAGAACAAG　6836

Qy　127　ThrLysGlnAlaAlaGluLeuProMetValIleCysGlyAsnLysAsnAspHisGlyGlu　146
Db　6837　ACCAAGCAGGCGGCGGAGCTGCCCATGGTCATCTGTGGCAACAAGAACGACCACGGCAG　6896

Qy　147　LeuCysLysArgGlnValProThrThrGlyAlaGluLeuLeuValSerGlyAspAspLeuSerPhe　166
Db　6897　CTGTGCCGCCAGGTGCCCACCACCGGCCGAGCTGCTGGTGTCGGGCGACGAGAACTGC　6956

Qy　167　AlaTyrPheGluValSerAlaLysAspSerThrAsnValAspGluMetPheTyrValLeu　186
Db　6957　GCCTACTTCGAGGTGTCGGCCAAGAAGAACACCAACGTGGACGAGATGTTCTACGTGCTC　7016

Qy　187　PheSerMetAlaLysLeuProHisGluMetSerProAlaLeuHisArgLysIleSerVal　206
Db　7017　TTCAGCATGGCCAAGCTGCCACACGAGATGAGCCCCGCCCTGCATCGCAAGATCTCCGTG　7076

RESULT 5

US-09-709-103-1

; Sequence 1, Application US/09709103
; Patent No. 6733991
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/709,103
; CURRENT FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1

; SEQ ID NO 1
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(843)
; OTHER INFORMATION:

US-09-709-103-1

Alignment Scores:
Pred. No.:
Score: 9.22e-112
Percent Similarity: 77.70%
Best Local Similarity: 61.87%
Query Match: 63.83%

Length: 846
Matches: 172
Conservative: 44
Mismatches: 46
Indels: 16
Gaps: 4

US-09-778-963B-2 (1-266) x US-09-709-103-1 (1-846)

RESULT 6

US-09-439-410A-1

; Sequence 1, Application US/09439410A
; Patent No. 6746852
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 1919/60388-B
; CURRENT APPLICATION NUMBER: US/09/439,410A
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin version 3.1

; SEQ ID NO 1
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(843)
; OTHER INFORMATION:

US-09-439-410A-1

Alignment Scores:
Pred. No.:
Score: 9.22e-112
Percent Similarity: 77.70%
Best Local Similarity: 61.87%
Query Match: 63.83%

Length: 846
Matches: 172
Conservative: 44
Mismatches: 46
Indels: 16
Gaps: 4

US-09-778-963B-2 (1-266) x US-09-439-410A-1 (1-846)

RESULT 7

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Qy    61  AsnIleArgGlyAspMetTyrGlnLeuAspThrSerGlyAsnHisProPhe      80
Db   196  TCCATCCGCGGCGGGGAGGTCTACGAGTTGGACATCCTCGACACGTCCGGCAACCACCCTTC  255

Qy    81  ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu    100
Db   256  CCCGCCATGCGGCGCCTCTCATCCTCACAGGAGACGGTTTCATCCTGGTGTTCAGTCTG     315

Qy   101  AspAspAsnArgGluSerPheAspGluValValLysArgLeuGlnIleLeuGluValLys    120
Db   316  GACAACCGCGACTCCTTCGAGGAGGTCGAGCGGCTCCAGGCAGCACAGGCAAG         375

Qy   121  SerCysLeuLysAsnLysThrLysGlyLeuAlaLaAlaGluLeuProMetValIleCysGlyAsn 140
Db   376  TCTTGCCTCAAGAACAAAAACCAAGGAGAACGGTGGCCGTCATCTGCGGCAAC         435

Qy   141  LysAsnAspHisGlyGluLeuCysArgGlnValValProThrThrGlyAlaGluLeuLeuVal 160
Db   436  AAGGGTGACCGC---GACTTCTACCGCGGAGGTGGACCGGAGGAGATCCGAGCAGCTGGTG   492

Qy   161  SerGlyAsp---GluAsnSerAlaTyrPheGluValSerAlaLysGlyAsnThrAsnVal    179
Db   493  GGCGACGACCCCGCGCGGCTCTTCGAGATCTCGCCGAAGAACGGAAGCACCAGCCTG      552

Qy   180  AspGluMetPheTyrValLeuPheSerMetAlaLysTyrLeuProHisGluMetSerProAla 199
Db   553  GACCAGATGTTCCGCGCGGCTCTTCGCCATTGGCCAAGTTGCACAGCCGAGATGAGCCCAGAC 612

Qy   200  LeuHisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCysMet    219
Db   613  CTGCACCGCAAGGTCTCGGTGCAGTACTGCGACGCCTTCCATCCGCGGCCGTTCTGCATG   666

Qy   220  ArgArgValLysGluMet----------------------------------AspAla    227
Db   667  CGGAACAGAAGCTGCTGGGGGGCCGGGGGCGGGGGGGGGGGGACCCGGGGCGACGCC     726

Qy   228  TyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrTyrIle 247
Db   727  TTTGGCATGGTGGCACCCTTCGCGCGCCGCCCAGCGTACACAGCGACCTCATGTACATC   786

Qy   248  LysAlaLysValLeuArgGluGlyGlnAlaArgGluArgAspLysCysThrIle         265
Db   787  CGCGAGAAGGCCCAGCGCGCCCAAGGACCAAGAGGAGCGCTGCGTCATC             840
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Alignment Scores:
Pred. No.:	
Score:	3.03e-111
	879.00
Percent Similarity:	77.70%
Best Local Similarity:	61.87%
Query Match:	63.83%

Length:	1740
Matches:	172
Conservative:	44
Mismatches:	46
Indels:	16

DB:
US-09-778-963B-2 (1-266) x US-09-709-103-45 (1-1740)

Gaps: 4

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Qy     1  MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr    20
Db   161  ATGATCAAGAGAGATGTGCCCGAGCAGACTCGGAGCTGAGTATCCGGCAGAACTGCTAT    220

Qy    21  ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu    40
Db   221  CGGATGGTCATCCTCGGCGTCCAAGGTGGGGCAAGACGGCCATCGTGTCGCGGTTCCTC   280

Qy    41  AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr   60
Db   281  ACCGGACGCTTCGAGGACCAGTACACGCCTACCATCGAGGACTTCCACCGCAAGGTCTAC  340

Qy    61  AsnIleArgGlyAspMetTyrGlnLeuAspThrSerGlyAsnHisProPhe           80
Db   341  TCCATCCGCGGCGGGGAGGTCTACGAGTTGGACATCCTCGACACGTCCGGCAACCACCCGTTC 400

Qy    81  ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu   100
Db   401  CCCGCCATGCGGCGCCTCTCATCCTCACAGGAGACGGTTTCATCCTGGTGTTCAGTCTG    460

Qy   101  AspAspAsnArgGluSerPheAspGluValValLysArgLeuGlnIleLeuGluValLys   120
Db   461  GACAACCGCGACTCCTTCGAGGAGGTCGAGCGGCTCCAGGCAGCACAGGCCTG         520

Qy   121  SerCysLeuLysAsnLysThrLysGlyLeuAlaAlaAlaGluLeuProMetValIleCysGlyAsn 140
Db   521  TCTTGCCTCAAGAACAAAAACCAAGGAGAACGGTGGCCGTCATCTGCGGCAAC         580

Qy   141  LysAsnAspHisGlyGluLeuCysArgGlnValValProThrThrGlyAlaGluLeuLeuVal 160
Db   581  AAGGGTGAC---GACTTCTACCGCGGAGGTGGACCGGAGGAGATCCGAGCAGCTGGTG     637

Qy   161  SerGlyAsp---GluAsnSerAlaTyrPheGluValSerAlaLysGlyAsnThrAsnVal  179
Db   638  GGCGACGACCCCGCGCGGCTCTTCGAGATCTCGCCGAAGAACGGAAGCACCAGCCTG      697

Qy   180  AspGluMetPheTyrValLeuPheSerMetAlaLysTyrLeuProHisGluMetSerProAla 199
Db   698  GACCAGATGTTCCGCGCGGCTCTTCGCCATTGGCCAAGTTGCACAGCCGAGATGAGCCCAGAC 757

Qy   200  LeuHisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCysMet    219
Db   758  CTGCACCGCAAGGTCTCGGTGCAGTACTGCGACGCCTTCCATCCGCGGCCGTTCTGCATG   811

Qy   220  ArgArgValLysGluMet-----------------------------------AspAla    227
Db   812  CGGAACAGAAGCTGCTGGGGGGCCGGGGGGCGGGGGGGGGGGACCCGGGGCGACGCC      871

Qy   228  TyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrTyrIle 247
Db   872  TTTGGCATGGTGGCACCCTTCGCGCGCCGCCCAGCGTACACAGCGACCTCATGTACATC   931

Qy   248  LysAlaLysValLeuArgGluGlyGlnAlaArgGluArgAspLysCysThrIle        265
Db   932  CGCGAGAAGGCCCAGCGCGCCCAAGGACCAAGAGGAGCGCTGCGTCATC            985
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; SEQ ID NO 45
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (146)..(988)
; OTHER INFORMATION:
US-09-439-410A-45

Alignment Scores:
Pred. No.:
Score: 3.03e-111
Percent Similarity: 77.70%
Best Local Similarity: 61.87%
Query Match: 63.83%
DB: 4

Length: 1740
Matches: 172
Conservative: 44
Mismatches: 46
Indels: 16
Gaps: 4

US-09-778-963B-2 (1-266) x US-09-439-410A-45 (1-1740)

Qy   1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
            ||| ::| ||||| | |:   ::
Db   161 ATGATGAAGAAGAATGTGCCCAGCGACTCGGAGCTATCCCGGCCAAGAACTGCTAT 220

Qy   21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
            |||:|||||||||||||||| |||:::||||||||||||||||||||||||||||||
Db   221 CGCATGGTCATCCTCGGCTCGTCCAAGGTGGGCAACGGCCATCGTGTCCGCGCTTCCTC 280

Qy   41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr 60
            |||||| :| |||:||||||||||:|||:||| ||||||:||||||||||||||
Db   281 ACCGGCCGCTTCGAGGACGGCCTACACGCCTACCATGAGGACTTCCACCGGAGTTCTAC 340

Qy   61 AsnIleArgGlyAspMetTyrGlnLeuLeuAspThrSerGlyAsnHisProPhe 80
            ::|||:||||||||||||| ||||||| |||||:|||||||||||||||||||||
Db   341 TCCATCCGCGGCGAGGTCTACCAGTCGCAGATCCTCGACACGTCCGGCAACCCGGTTC 400

Qy   81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuLeuValPheSerLeu 100
            :::|||||||||| ||| ||: ||||||| ||::: |||:
Db   401 CCCGGCCATGCGGCGGCTCTCCATCCTCACAGGAGACGTTTTCATCCTGGTGTTCAGTCTG 460

Qy   101 AspAsnAsnArgGluSerPheAspGluValGlyLysGlnIleIleLeuGluValLys 120
            |||||||||| ::: |||||||||||||||||||:::||||||||:
Db   461 GACAACCGCGACTCCTTCGAGGAGGTGGCAACGCAGATCATCCTCGACACCAAG 520

Qy   121 SerCysSerLeuLysSerAsnLysThrLysGluAlaLeuAlaGluLeuProMetValIleCysGlyAsn 140
            |||||| |||||||:::| ||||||||||:::|:   :::
Db   521 TCTTGCTCCAAGAACAAAACCAAGGAAGCGCTGGCGGAGCTGCCCATGGTCATCTGCGGCAAC 580

Qy   141 LysAsnAspHisGlyLeuCysArgGlnVal 160
            ||||||::: |:|||||||||||||||||
Db   581 AAGGGTGACCGC--GACTTCTACCGCGAGGTGAACGGCCAGCGGGTG 637

Qy   161 SerGlyAsp---GluAsnSerAlaTyrArgPheGluValSerAlaLysLysAsnThrAsnVal 179
            ::: |||||||||:::
Db   638 GGCGACGACCCCCACGCGTCGCCCTACTTCGAGATCTCGGCCAAGAAGAACAGCAGCCTG 697

Qy   180 AspGluMetPheTyrValLeuProHisGluMetSerProAla 199
            ::||||||||| |||
Db   698 GACCAGATGTTCCCGCGGCTCTTCGCCATGGCCAAGCCGGAGATGAGCCCGAC 757

Qy   200 LeuHisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCysMet 219
            ::||||||||||
Db   758 CTGCACCGCAAGGTCTCGGTTCAGTACTGCGACGTGCCCTGGCACAAGGAG-----GCGCTG 811

Qy   220 ArgArgValLysGluMet---------------------AspAla 227
            |||||||||||||||
Db   812 CGGAGACAAGAGCTGCTCGGGCGGCGGCGCCGGGGGGGGGGCGGGGCCAGCG 871

Qy   228 TyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrIle 247
            ::|||||||||||
Db   872 TTTGGCATCGTGGCACCCTTCGCGCGGCGGCCCAGCGTACAGCGACCTCATGTACATC 931

Qy   248 LysAlaLysValLeuArgGluGlyGlnAlaArgGluArgAspLysCysThrIle 265
            |||||||||||
Db   932 CCCGGAGAAGGCCAGGCCCGGGCGGCAGCGCAAGGACAAAGGAGGCGCTGCGGTCATC 985

RESULT 9
US-09-709-103-3
Sequence 3, Application US/09709103
Patent No. 6733991
GENERAL INFORMATION:
APPLICANT: Cismowski, Mary
APPLICANT: Duzic, Emir
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
FILE REFERENCE: 60388-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/709,103
CURRENT FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1

; SEQ ID NO 3
; LENGTH: 1801
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)..(996)
; OTHER INFORMATION:
US-09-709-103-3

Alignment Scores:
Pred. No.:
Score: 3.21e-111
Percent Similarity: 77.70%
Best Local Similarity: 61.87%
Query Match: 63.83%
DB: 4

Length: 1801
Matches: 172
Conservative: 44
Mismatches: 46
Indels: 16
Gaps: 4

US-09-778-963B-2 (1-266) x US-09-709-103-3 (1-1801)

Qy   1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
            ||| ::| ||||| | |:   ::
Db   169 ATGATGAAGAAGAATGTGCCCCAGCGACTCGGAGCTATCCCGGCCAAGAACTGCTAT 228

Qy   21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
            |||:|||||||||||||||| |||:::||||||||||||||||||||||||||||||
Db   229 CGCATGGTCATCCTCGGCTCGTCCAAGGTGGGCAACGGCCATCGTGTCCGCGCTTCCTC 288

Qy   41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr 60
            |||||| :| |||:||||||||||:|||:||| ||||||:||||||||||||||
Db   289 ACCGGCCGCTTCGAGGACGGCCTACACGCCTACCATGAGGACTTCCACCGGAGTTCTAC 348

Qy   61 AsnIleArgGlyAspMetTyrGlnLeuLeuAspThrSerGlyAsnHisProPhe 80
            ::|||:||||||||||||| ||||||| |||||:|||||||||||||||||||||
Db   349 TCCATCCGCGGCGAGGTCTACCAGTCGCAGATCCTCGACACGTCCGGCAACCCGGTTC 408

Qy   81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuLeuValPheSerLeu 100
            :::|||||||||| ||| ||: ||||||| ||::: |||:
Db   409 CCCGGCCATGCGGCGGCTCTCCATCCTCACAGGAGACGTTTTCATCCTGGTGTTCAGTCTG 468

Qy   101 AspAsnAsnArgGluSerPheAspGluValGlyLysGlnIleIleLeuGluValLys 120
            |||||||||| ::: |||||||||||||||||||:::||||||||:
Db   469 GACAACCGCGACTCCTTCGAGGAGGTGGCAACGCAGATCATCCTCGACACCAAG 528

Qy   121 SerCysSerLeuLysSerAsnLysThrLysGluAlaLeuAlaGluLeuProMetValIleCysGlyAsn 140
            |||||| |||||||:::| ||||||||||:::|:   :::
Db   529 TCTTGCTCCAAGAACAAAACCAAGGAAGCGCTGGCGGAGCTGCCCATGGTCATCTGCGGCAAC 588

Qy   141 LysAsnAspHisGlyLeuCysArgGlnValProThrThrGluLeuLeuVal 160
            ||||||::: |:|||||||||||||||||
Db   589 AAGGGTGACCGC--GACTTCTACCGCGAGGTGAACGGCCAGCGGGTG 645

Qy   161 SerGlyAsp---GluAsnSerAlaTyrArgPheGluValSerAlaLysLysAsnThrAsnVal 179
            ::: |||||||||:::
Db   646 GGCGACGACCCCCACGCGTCGCCCTACTTCGAGATCTCGGCCAAGAAGAACAGCAGCCTG 705

Qy   180 AspGluMetPheTyrValLeuProHisGluMetSerProAla 199
            ::||||||||| |||
Db   706 ...

RESULT 10
US-09-439-410A-3
; Sequence 3, Application US/09439410A
; Patent No. 6746852
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 1919/60388-B
; CURRENT APPLICATION NUMBER: US/09/439,410A
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 1801
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)..(996)
; OTHER INFORMATION:
US-09-439-410A-3

Alignment Scores:

Pred. No.:		
Score:	3.21e-111	
	879.00	Length: 1801
Percent Similarity:	77.70%	Matches: 172
Best Local Similarity:	61.87%	Conservative: 44
Query Match:	63.83%	Mismatches: 46
DB:	4	Indels: 16
		Gaps: 4

US-09-778-963B-2 (1-266) x US-09-439-410A-3 (1-1801)

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Qy     1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
           ||||   |||  |:|
Db   169 ATGATGAAGAGAAGATGTGCCCAGAAGCGACTCGGAGCTGAGTATCCCGGCCAAGAACTGCTAT 228

Qy    21 ArgMetValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
           |||||||||:||:
Db   229 CGCATGGTCATCCTCGGCTCGTCCAAGGTGGGCAAGACGGCCATCGTGTCGCGGCTTCCTC 288

Qy    41 AsnGlyArgPheGluAspAsnGlnThrProThrIleGluAspPheHisArgLysValTyr 60
           ::|||||:|
Db   289 ACCGGCCGGTTCGAGCAGCGCTACACCGCCTACCATCGAAGACTTCCACCGCAAGGTTCTAC 348

Qy    61 AsnIleArgGlyAspMetTyrGlnLeuAspThrSerGlyAsnHisProPhe 80
           ::|||||||||:|
Db   349 TCCATCCGCGGCGAGTCTACACGCACATCCCCGACCACCACCCGTTC 408

Qy    81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheSerLeu 100
           ||||||||||||||||
Db   409 CCCGCCATGCGGCGCCTCTCCATCCTCACAGGAGACGTTTTCATCCTGGTTCAGTTCTG 468

Qy   101 AspAsnArgGluSerPheAspGluValLysArgLeuGlnIleLeuGluValLys 120
           ||||||
Db   409 CCCGCCATGCGGCGCCTCTCCATCCTCACAGGAGACGTTTTCATCCTGGTTCAGTTCTG 468

Qy   141 LysAsnAspHisGlyGluLeuCysArgGlnValProThrThrGluValLeuLeuVal 160
           |||   |:|
Db   589 AAGGGTGACCGC---GACTTCTACCCGCGAGGTGGCACGCGCGGAGATCGAGCAGCTGGTG 645

Qy   220 ArgArgValLysGluMet------ 227     AspAla 227
           ||||   |||
Db   766 CTGCACCGCAAGGTCTCGGTGCAGACTGGTGGCGACGTGCCTCACAACGAGAAG------GCCCTG 819

Qy   228 TyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrIle 247
           ||||||:|
Db   880 TTTGGCATGGTGTCGCACCCTTCGGCGCGGCGGCCAAGGCTACACAGCGACCTCATGTACATC 939

Qy   248 LysAlaLysValLeuArgGluGlyGlnAlaArgGluArgAspLysCysThrIle 265
           |||
Db   940 CGCGAGGAGGCCAGCGCGGCGGGCCAAGGACAAGGACGCGCTGCGTCATC 993
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RESULT 11
US-09-053-374A-1
; Sequence 1, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 255..1097

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Db   469 GACAACCCGACACTCCTTCGGAGGAGGTGGCAGCGGCTCAGGCAGCAGAGTATCCTCGACACCAAG 528

Qy   200 LeuHisArgLysIleSerValGlnThrGlyGlyAspAlaPheHisProArgProPheCysMet 219
           ||||||   |:|   :::
Db   529 TCTTGCCTCCAAGAACAAAACCAAGGAGACGTGCCCCTTGGTCATCCTGGCCAAC 588

Qy   220 ArgArgValLysGluMet------                                    AspAla 227
           |||||||| |:|
Db   766 CTGCACCGCAAGGTCTCGGTGCAGACTGGTGGCGACGTGCCTCACAACGAGAAG------GCCCTG 819

Qy   141 LysAsnAspHisGlyGluLeuCysArgGlnValProThrThrGluValLeuLeuVal 160
           |||   |:|
Db   820 CGGAACAAGAAGCTGCTGCGGGGCGGCGGCGGGCGGGGCGGGGACGCC 879

Qy   161 SerGlyAsp---GluAsnSerAlaTyrPheGluValSerAlaAlaTyrAsnVal 179
           :::|||
Db   646 GGCGACGACCCCCAGCCCTACTTCGAGGTGTCCGCGGCCTACAACGCCAGCGTG 705

Qy   180 AspAspGlnMetPheTyrValLeuPheSerMetAlaLysGluLeuProHisGluMetSerProAla 199
           ||| ||||||
Db   706 GACCAGATGTTCCGCGTGCTCTTCGCCATGGCCAAGGTGCCCCACGAGATGAGCCCAGAC 765

Qy   228 TyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrIle 247
           ||||||
Db   880 TTTGGCATGGTGTCGCACCCTTCGGCGCGGCGGCCAAGGCTACACAGCGACCTCATGTACATC 939

Qy   248 LysAlaLysValLeuArgGluGlyGlnAlaArgGluArgAspLysCysThrIle 265
           |||
Db   940 CGCGAGGAGGCCAGCGCGGCGGGCCAAGGACAAGGACGCGCTGCGTCATC 993
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Left column

RESULT 12
US-09-053-374A-4
; Sequence 4, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:

US-09-778-963B-2 (1-266) x US-09-053-374A-1 (1-1841)

Alignment Scores:
Pred. No.:
Score:　　　　　　　　　　3.33e-111
　　　　　　　　　　　　　879.00
Percent Similarity:　　　77.70%
Best Local Similarity:　63.83%
Query Match:

Length:　　　　1841
Matches:　　　172
Conservative:　44
Mismatches:　46
Indels:　16
Gaps:　4

```
Qy    1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr   20
          ||||||:|    ::|      ::|||||:||||||||||:||||:|||||||||
Db  270 ATGATCAAGAAGATGTGCCCAAGGGACTCGGAGTATCCCGGCCAAGAAGACTGCTAT  329

Qy   21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu   40
          |||||||:||||||:||||:||||:||||||||||:|||||||||:||::|||||
Db  330 CGCATGGTCATCCTCGGCGCTCGGTCCAAGGTGGGCAAGACGGCCATCGTGTCCCGCTTC  389

Qy   41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr   60
          |||||||||||:|||||||||||:||||||||||||||||:||||||||||:|||
Db  390 ACCGGCGCCTTCGAGGAGCAGTACACCCCTACCATCGAGGACTTCCACCGGAAGTTCTAC  449

Qy   61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe   80
          :|||:||||:||||:||||||||||||||||:||||||||||||||:||||||||
Db  450 TCCATCCGCGGCGAGTCTACCAGCTCGACACATCCTCGGCCAACACCACCCGTTC  509

Qy   81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu  100
          |||||||||:|||:||:|||:|||||:||||:||||||||:||||||||||:|||
Db  510 CCCGCCATGCGCCGCCTCTCCATCCTCACAGGAGACGTTTTCATCCTGGTGTTCAGTCTG  569

Qy  101 AspAsnArgGluSerPheAspGluIleLysArgLeuGlnIleLeuLeuGluValVal  120
          :|||||||||:|||||::|||||||||||:|||||::|||||:|||:|||
Db  570 GACAACCGCGACTCCTTCGACGAGGTGCAGCGACTCCTCGAACCACCAAG  629
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Qy  121 SerCysGluLeuLysAsnLysThrLysGluAlaAlaLeuGluProMetValIleCysGlyAsn  140
          |||:|||||||||||||:|||||||:||||||||:|||||||||||:
Db  630 TCTTGCCTCAAGAACAAAACCAAGGAGGCGGCCCTGGAGCCCATGGTCATCTGCGGCAAC  689

Qy  141 LysAsnAspHisGlyGluLeuGlnValProThrHisGlnLeuAlaGluLeuLeuVal  160
          :||:|     ||::|||||||:|||||
Db  690 AAGGGTGACCGC--GACTTCTACCCGGAGGTGGACCAGATCGGAGCAGTGGTG  746

Qy  161 SerGlyAsp---GluAsnSerAlaLeuTyrPheGluValSerAlaLysLysAsnThrAsnVal  179
          :|||
Db  747 GGCGACGACCCCCAGGCTGGGCCTACTTCGAGGTGTCGGCCAAGAAGAACAGCAGCCTG  806

Qy  180 AspGluMetThrTyrValLeuPheSerMetAlaLysLeuGluProHisGluMetSerProAla  199
          :|| ::|
Db  807 GACCAGATGTTCCGCGGCGCTCTCCCCATGGGCCATGGAGAGCCCAGAC  866

Qy  200 LeuHisArgLysIleSerValGlnTyrGlyAspAlaProHisProArgProCysSerMet  219
          :|||                          ::|
Db  867 CTGCACCGGAAGGTCTCGGTGCAGTACTGCGACGCTGCCACAAGAAG------  920

Qy  220 ArgArgValLysGluMet-----------------------AspAla  227
          :||                          ::|
Db  921 CGGACAAGAGAGCTGCTGCGGCGGCGGCGGCGGGGGCGACCCGGGGGCGACCGC  980

Qy  228 TyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysThrIle  247
          :||:::||||||||||||||||:
Db  981 TTTGGCCATCCTGTGGCCAccCCTTCGCGCGCCGCGGGGTACACAGCGACCTTCAGTACATC  1040

Qy  248 LysAlaLysValLeuArgGlyGluGlyArgAspLysCysThrIle  265
          :|||||||||||||||||:||||||||||:
Db 1041 CGCGAGAGGAGGCCACGGCCAGCCAAGGAGGAGAGCCTGCCGTCATC  1094
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Right column

US-09-778-963B-2 (1-266) x US-09-053-374A-4 (1-1689)

Alignment Scores:
Pred. No.:
Score:　　　　　　　　　　6.41e-111
　　　　　　　　　　　　　876.50
Percent Similarity:　　　77.98%
Best Local Similarity:　63.65%
Query Match:

Length:　　　　1689
Matches:　　　171
Conservative:　45
Mismatches:　46
Indels:　15
Gaps:　4

```
Qy    1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr   20
          ||||||:|    ::|      ::|||||:||||||||||:||||:|||||||||
Db  147 ATGATCAAGAAGATGTGCCCAAGGGACTCGGAGTATCCCGGCCAAGAAGACTGCTAC  206

Qy   21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu   40
          |||||||:||||||:||||:||||:||||||||||:|||||||||:||::|||||
Db  207 AGGATGGTCATCCTCGGCGCTCGGTCCAAGGTGGGCAAGACGGCCATCGTGTCGGGCTTC  266

Qy   41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr   60
          |||||||||||:|||||||||||:||||||||||||||||:||||||||||:|||
Db  267 ACGGGCCGCTTCGAGGACGAGTACACCCCTACCATCGAGGACTTCCACCGGAAGTTTTAC  326

Qy   61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe   80
          :|||:||||:||||:||||||||||||||||:||||||||||||||:||||||||
Db  327 TCGATCCGCGGCGACATGTACCAGTTGGACATACCTCGGCAATCATCCGTTT  386

Qy   81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu  100
          |||||||||:|||:||:|||:|||||:||||:||||||||:||||||||||:|||
Db  387 CCCGCCATGCGCCGGCTCTCCATCCTCACAGAGACGTTTTCATCCTGGTGTTCAGTTTA  446

Qy  101 AspAsnArgGluSerPheAspGluIleLysArgLeuGlnIleLeuLeuGluValVal  120
          :|||||||||:|||||::|||||||||||:|||||::|||||:|||:|||
Db  447 GACAACCGCGACTCCTTCGACGAGGTGCAAAGGCTCAAACACCAGGATCCTAGACACAAG  506

Qy  121 SerCysGluLeuLysAsnLysThrLysGluAlaAlaLeuGluProMetValIleCysGlyAsn  140
          |||:|||||||||||||:|||||||:||||||||:|||||||||||:
Db  507 TCCTGTGCTCAAGAACAAAACCAAGGAGGCGGCCCTGGAGCCCATTGCGGTAAC  566
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Alignment Scores:

Pred. No.:	1.2e-102
Score:	820.00
Percent Similarity:	66.56%
Percent Identity:	52.63%
Best Local Similarity:	59.55%
Query Match:	59.55%
DB:	3

Length:	3079	Matches:	170
Conservative:	45	Mismatches:	47
Indels:	62	Gaps:	5

US-09-053-374A-6

MOLECULE TYPE: DNA (genomic)
TOPOLOGY: linear
STRANDEDNESS: single
TYPE: nucleic acid
LENGTH: 3079 base pairs
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 6:
REFERENCE/DOCKET NUMBER: A-514
REGISTRATION NUMBER: 31,602
NAME: COOK, ROBERT R.
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
FILING DATE:
APPLICATION NUMBER: US/09/053,374A
CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
CLASSIFICATION:
COUNTRY: US
ZIP: 91320
STATE: CA
CITY: THOUSAND OAKS
STREET: ONE AMGEN CENTER DRIVE
ADDRESSEE: AMGEN INC.
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 9
TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
APPLICANT: YEN, KWANG-MU
GENERAL INFORMATION:
Patent No. 6462177
Sequence 6, Application US/09053374A
US-09-053-374A-6
RESULT 13

Qy 141 LysAsnAspHisGlyGluLeuCysArgGlnValProThrThrGluAlaGluLeuLeuVal 160
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Db 567 AAAGGGGAGGACCGG---GACTTCTACCGCGAAGTGGAGCAGCGGGAGATTGAGCAGCTGGTG 623

Qy 161 SerGlyAsp---GluAsnSerAlaTyrPheGluValSerAlaLysLysAsnThrAsnVal 179
        ||| :::
Db 624 GGCGATGACCCTCAGGGTGTGCCTACTACTTCAGATATCTCCGGCAGAGATGAGAATAGCAGCCTG 683

Qy 180 AspGluMetPheTyrValLeuPheSerMetAlaLysLeuProHisGluMetSerProAla 199
        ||| :::|||
Db 684 GACCAGATGTTCTGTGGCTCTTTGCCATGGCCAAGCTGCCTCAGCGAGTGAGAGATGAGCCCTGAC 743

Qy 200 LeuHisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCysMet 219
        ||| :::
Db 744 TTGCACGGCAGGGTGTCTCTGCAGTACTGTGACGTGCTGCACAAAAAG------GCTCTG 797

Qy 220 ArgArgValLysGluMet------ 228
        ||| :::   :::
Db 798 AGGAACAAGAGAGCTTCTGCGTGCGGCGCGGGGGGGGCCGAGGTGGGGGCGACCGAGG AspAlaTyr 228

Qy 229 GlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrIleLys 248
        ||| :::
Db 858 GGCATCTTGGCGCCCTTTGCCTCGCGACCTAGCGTGCATAGCGACCTCATGTACATTCGT 917

Qy 249 AlaLysValLeuArgGluGlyGlnAlaLeuArgGlnAspLysCysThrIle 265
        ||| :::
Db 918 GAGAAAACCAGTGTCACCAGCCAGGCTTAAGGACAGAAGAGGCGCTGTGTCATC 968

US-09-778-963B-2 (1-266) x US-09-053-374A-6 (1-3079)

Qy   1 MetMetTyrThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
        ||| :::   :::
Db 318 ATGATCAAGAGAGATGTGGCCAAGCGACTCGAACTGGAGTATCCCGGCAGGAACTGCTAC 377

Qy   21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
        ||| :::
Db 378 AGGATGGTCATCCTCGGCGTCATCCAAAGTGGGGCAAGACGGCCATCGTGTCGGCCTTCTC 437

Qy   41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgGlyValTyr 60
        ||| :::
Db 438 ACGGGGCGGCTTCGAGGACCAGTATACACCCACCATTGAAGACTTCCACCGAGGAGTTTAC 497

Qy   61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
        ||| :::
Db 498 TGAATCCCGGCGGGGACATGTACCAGTTGGACATACTCGGACACATCTGGCCAATCATCCGGTTT 557

Qy   81 ProAlaMetArgArgLeuSerIle------ 88
        ||| :::
Db 558 CCCGCCATGCGGCCTCTCATCCTCACAGGTGAGTGGGGGGACCAGGACCGGTGGG 617

Qy   88 ------ 88
Db 618 GAGGGAATCTGCGGGAGCGGATGGGGCGGGGTGTGTTGTTGGCTGGTGTTCTGCT 677

Qy   88 ------ 88
Db 678 GCTCCGTGCTTGGCAGCTGCCCTCACCTTCCACTCGTTCCCCGTTGTA-GGAGACGTTTC 736

Qy   89 ------LeuThrGlyAspValPhe 94
        |||
Db 737 ATTCTGGTTGTTCAGCTTAGACAACCGCGACTCCTTCGAGGAGTTCGGAGGATCTCGGGCC 796

Qy   95 IleLeuValPheSerLeuValAsnAsnArgGluSerPheAspAsnValValGlyLysGlyLys 114
        ||| :::
Db 797 CAGATCCTAGACACCAAGTCCTGTGTCTCGAAGAACAAAACCAAAGAGAATGTGACGTGCCG 856

Qy 115 GlnIleLeuLeuGluValLysSerCysLeuLeuLysAsnLysLysGlyValAlaAlaGluLeuPro 134
        ||| :::
Db 857 CTGGTCATTTGCGGTAACAAAGGGGACGGG---GACTTCTACCGCGAAGTGGAGCAGCGGG 913

Qy 135 MetValIleCysGlyAsnAsnAspHisGlyGluLeuCysArgGlnValProThrThr 154
        ||| :::
Db 914 GAGATTGAGCAGCTGGTGGGCGATGACCCTCAGGGTGTGCCTACTACTTCAGATATCTCCGG 973

Qy 155 GluAlaGluLeuLeuValSerGlyAsp---GluAsnSerAlaTyrrPheGluValSerAla 173
        ||| :::   :::
Db 974 AAGAGAGAATAGCAGCCTGGACCAGATGTTCCGTGGCGCTCTTTGCCATGGCCAAGCTGCCT 1033

Qy 174 LysLysAsnThrAsnValAspGluMetPheTyrValLeuPheSerMetAlaLysLeuPro 193
        ||| :::
Db 1034 ACGGAGTGAGAGATGAGCCCTGACTTGCACGGCAGGGTGTCTCTGCAGTACTGTGACGTGCC 1093

Qy 194 HisGluMetSerProAlaLeuHisArgLysIleSerValGlnTyrGlyAspAlaPheHis 213
        ||| :::
Db 1093 ACGGAGATGAGCCCTGACTTGCACGGCAGGGTGTCTCTGCAGTACTGTGACGTGCTGCAC 1093

Qy 214 ProArgProPheCysMetArgArgValLysGluMet------ 225
        ||| :::
Db 1094 AAAAAG------GCTCTGAGGAACAAGAGAGCTTCTGCGTGCGGCGCGTGAAGAGTGGGGGC 1147

Qy 226 ------AspAlaTyrGlyMetValSerProPheAlaArgArgProSerValAsnSer 242
        ||| :::
Db 1148 GACCACGGAGATGCCTTTGGCATCTTGGCGCCCTTTGCCTCGCGACCTAGCGTGAATAGC 1207

Qy 243 AspLeuLysTyrIleLysAlaLysValLeuArgGluGlyGlnAlaLeuArgGlnAspLys 262
        ||| :::
Db 1208 GACCTCATGTACATTCGTGAGAAAACCAGTGTCACCAGCCAGGCTTAAGGACAGAAGAGGC 1267

Qy 263 CysThrIle 265
        |||
Db 1268 TGTGTCATC 1276

RESULT 14
US-09-053-374A-3
; Sequence 3, Application US/09053374A

; Patent No. 6462177
; GENERAL INFORMATION:
;   APPLICANT: YEN, KWANG-MU
;   TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: AMGEN INC.
;   STREET: ONE AMGEN CENTER DRIVE
;   CITY: THOUSAND OAKS
;   STATE: CA
;   COUNTRY: US
;   ZIP: 91320
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/053,374A
;   FILING DATE:
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: COOK, ROBERT R.
;   REGISTRATION NUMBER: 31,602
;   REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3986 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)

US-09-053-374A-3

Alignment Scores:
Pred. No.:   4.78e-102   Length: 3986
Score: 817.00   Matches: 172
Percent Similarity: 61.89%   Conservative: 44
Best Local Similarity: 49.28%   Mismatches: 46
Query Match: 59.33%   Indels: 87
DB: 3   Gaps: 5

US-09-778-963B-2 (1-266) x US-09-053-374A-3 (1-3986)

Qy   1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
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Db   789 ATGATCAAGAAGATGTGCCCGAGCGACTCGGAGCGTATCCCGGCCAAGAACTGCTAT 848

Qy   21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
           |||||||||||||:||||||||:||||||||:||||||||::||
Db   849 CGCATGGTCATCCTCGGCGCTCGTCCAAGGTGGGCCAAGAACGGCCATCGTGTCGCGGCTTCCTC 908

Qy   41 AsnGlyArgPheGluAspGlnThrTyrThrProThrIleGluThrAspPheHisArgGlyValTyr 60
           |||||||||||||:|||||||||:||||||:|||||||::|||
Db   909 ACCGGCGCGTTCGAGGACGGCCTACACGCTACCATCGAGACTTCCACGCAAGTTCTAC 968

Qy   61 AsnIleArgGlyAspMetTyrGlnLeuAspThrSerGlyAsnHisProPhe 80
           |:|||||||||||:||||
Db   969 TCCATCCGCGGCGAGCGGTCTACCAGCTCGACAATCCTCGGCCAACCACCCGTTC 1028

Qy   81 ProAlaMetArgArgLeuSerIleLeuThr---------------------------- 90
           ||||||||||||||||||||||||
Db 1029 CCCGCCATGCGGCGGCGCCTCTCCATCCTCACAGGTGAGCCGGGGGCCGCCGAGGTGCGGGGAG 1088

Db 1089 GGAGGGGCGGGGAACCCTCGGCGAGGCGGCGCGCCCCCCGCGTCCGGCCTGCTGCGCGC 1148

Db 1149 CGAGTAGTGCGGCTTCGCGCTTAGAGAGGCTAGCGCGGGCCCCCGCGGGCGGCCTTCAAAGTCAGCC 1208

Db 1209 CGACTTGTCCCTGGGCGGCCCCACCTTCACCTTCTCCTTTTCTGCTCTGTGCCCCTCT 1268

Qy   91 -GlyAspValPheIleLeuValPheSerLeuAspAsnArgGluSerPheAspGluValGly 110
           ||||||||||:|||||:||||||||||||||||:|
Db 1269 AGGAGACGTTTTCATCCTGGTGTTTCAGTCTCGGACAACCGCGACTTCCTTCGAGGAGGTGCA 1328

Qy   110 sArgLeuGlnIleGlnIleIleLeuValIleValGlySerCysLeuLysAsnLysThrLysGluVal 130
           |||||||:|:|||||:::|||||||:::|||
Db 1329 GCGGCTTCAGGCAGCAGGAGATCCTTGCACCAAGCTCTTGCCTCAAGAACAAAAACCAAGGAGAA 1388

Qy   130 aAlaGluLeuProMetValIleCysGlyAsnLysAsnAspHisGlyLeuLeuCysArgGl 150
           |||||||||||||||||||||||:||||:::::
Db 1389 CGTGGACGTGCCCCTGGTCATCTGCGGCAACAAGAACGACCATGGA---GACTTCTACCGCGA 1445

Qy   150 nValProThrThrGluValAlaGluLeuLeuValLeuSerGlyAlaTyrPh 169
           |||||||||||||||||||||||||||||:::
Db 1446 GGTGGACACCAGCGGACAATCGACGCACGCTGGTGGGCGCGA---GluAsnSerAlaTyrPh 1505

Qy   169 eGluValSerAlaLysGlyAsnThrAsnValAspGluMetPheTyrValLeuPheSerMe 189
           |||:||||||||||||||||:::
Db 1506 CGAGATCTCCGGCCCAAGAAGAACACAGAGCCTGGACGAGGAGTTCCGGGCGGCTCTTCGCCAT 1565

Qy   189 tAlaLysSerLeuProHisGluMetSerProAlaLeuHisArgGlyIleSerValGlnThrTyrGl 209
           |||||:|||||||||||||||||||||||||||:::||||:||||||||
Db 1566 GGCCAAGCTGCCCCACGAGATGAGCCCCAGCACCTGCACCGGAGGTCTCGGTGCAGTACTG 1625

Qy   209 yAspAlaPheHisProArgProPheCysMetArgArgValLysGluMet--------- 225
           ::|:|||| |||
Db 1626 CGACGTGCTGCACAACGAAG------GCGCTGCGGCGACAACAGAAGCTGCTGCGCGCAG 1679

Qy   226 ------------------AspAlaTyrGlyMetValSerProPheAlaArgAr 237
                              ||||:::|||||||||||:||:
Db 1680 CGGGCGCGGCGGGGGCGGCGGACGCGCCTTGGCATCGTGGCCACCCTTCGCGGCGGCCG 1739

Qy   237 gProSerValAsnSerAspLeuCysTyrIleLysAlaLysValLeuArgGluVtGlnAl 257
           |||||||||||:|||:||||||||:||||||||||:
Db 1740 GCCCAGCGTGAACAGCGACCTCATGTACATCCGGGCAAGCCAGCCGGGCGGCAGGC 1799

Qy   257 aArgGluArgAspLysCysThrIle 265
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Db 1800 CAAGGAACAAGGAGCGCCTGCCTCATC 1824

RESULT 15
US-09-439-410A-73
; Sequence 73, Application US/09439410A
; Patent No. 6746852
; GENERAL INFORMATION:
;   APPLICANT: Cismowski, Mary
;   APPLICANT: Duzic, Emir
;   TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
;   FILE REFERENCE: 1919/60388-B
;   CURRENT APPLICATION NUMBER: US/09/439,410A
;   CURRENT FILING DATE: 1999-11-11
;   NUMBER OF SEQ ID NOS: 118
;   SOFTWARE: Patentin version 3.1
; SEQ ID NO 73
;   LENGTH: 4990
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-439-410A-73

Alignment Scores:
Pred. No.:   6.92e-102   Length: 4990
Score: 817.00   Matches: 172
Percent Similarity: 61.89%   Conservative: 44
Best Local Similarity: 49.28%   Mismatches: 46
Query Match: 59.33%   Indels: 87
DB: 4   Gaps: 5

US-09-778-963B-2 (1-266) x US-09-439-410A-73 (1-4990)

Qy   1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20

Job time : 216 secs

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Qy    21  ArgMetValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu        40
Db  2978  CGCATGGTCATCCTCGGCTCATCCCGCGTCGGGCAAGAGCCATCGGTGTCCGGCTTCCTC    3037

Qy    41  AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgGlyLysValTyr  60
Db  3038  ACCCGCGCCTTCGAGGACGGCTACACGCCTACCATCGAGGACTTCCACCGGCAAGTTCTAC  3097

Qy    61  AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe     80
Db  3098  TCCATCCGCGGCGAGGTCTACCAGCTCGACATCCTCGACACGTCCGGCAACCACCCGTTC    3157

Qy    81  ProAlaMetArgArgLeuSerIleLeuThr------                             90
Db  3158  CCCGCCATGCGGCGCCTCTCCATCCTCACAGGTGAGCGGGGGCGGGGGCAGGTGCGGGAG    3217

Qy    90  ---                                                              90
Db  3218  GGAAGGGCGGGAACCTCGCCCAGGCGCCCCCGGAGCGGTCCGGCTGCCGCGCGC          3277

Qy    90  ---                                                              90
Db  3278  CGAGTAGTGCCTTCGCGCTTAGAGAGGCTAGCGCGCCCCCGGGGCCTCAAAGTCAGCC      3337

Qy    90  ---                                                              90
Db  3338  CGACTTGTCCCCTGGGGCGGCCACCCTCCACCTTCTCCTTTTCTGCTCTCTGTCCCCCTCT  3397

Qy    91  -GlyAspValPheIleLeuValPheSerLeuAspAsnArgGluSerPheAspGluValLy   110
Db  3398  AGGAGAACGTTTTCATCCTGGTGTTCAGTCTGGACAACCGCGAGTCCTTCGAGGAGTGCA    3457

Qy   110  sArgLeuGlnLysGlnIleIleLeuGluValValLySerCysGlyLeuLysGlyThrLysGlyLeuA  130
Db  3458  GCGGCTCAGGCGCAGATCCCTCGACACCAAGTCTTGCCTCAAGACAACAAAACCAAGGAGAA  3517

Qy   130  aAlaGluLeuProMetValIleLeuCysGlyAsnLysAsnAspHisGlyGluLeuCysArgGl  150
Db  3518  CGTGGACGTGCCCCTGTCATCTGCGGCCAACAAGGGTGACCGC---GACTTCTACCGCGA   3574

Qy   150  nValProThrThrGluValAlaGluLeuLeuValSerGlyAsp---GluAsnSerAlaTyrPh  169
Db  3575  GGTGGACCACGCGGAGATCGAGCAGCACTGGTCGGGCGACGACCCCCAGCGCGTGCGCTACTT  3634

Qy   169  eGluValSerAlaLysLysAsnThrAsnValAspGluMetPheTyrValLeuPheSerMe   189
Db  3635  CGAGATCTCGGCCAAGAAGAACAGAGCCCTGGACAGAGATGTTCCCGGCGCTTCTTCGCCAT  3694

Qy   189  tAlaLysLeuProHisGluMetSerProAlaLeuHisArgHisIleSerValGlnTyrGl   209
Db  3695  GGCCAAGCTGCCCAGCGAGATGAGCCCCGCACTGCACCGCAAGGGTCTCGGTGCAGTACTG  3754

Qy   209  yAspAlaPheHisProArgProPheCysMetArgArgValLysGluMet---------     225
Db  3755  CGACCGTGCTGCACAAGAAG------GCGCTGCGGAACAAGAGAGCTGCGGGCCGGCCGCAG  3808

Qy   226  ------AspAlaTyrGlyMetValSerProPheAlaArgAr                       237
Db  3809  CGGCGCGGCGGCGGCCCGGGACCCGGGCGACGCGCCTTTGGCATCGTGGCACCCTTCGCGCCCG  3868

Qy   237  gProSerValAsnSerAspLeuLysTyrIleLeuAlaLysValLeuArgGluGlyAl      257
Db  3869  GCCCAGCGTACACAGGCACCTCATGTACATCCGCGAGAAGGCCCAGCGGGCCCAGGC      3928

Qy   257  aArgGluArgAspLysCysThrIle  265
Db  3929  CAAGGACAAGGAGCGCGGCTGCGTCATC  3953
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Search completed: April 24, 2005, 07:39:47

OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: April 24, 2005, 05:50:40 ; Search time 631 Seconds
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2559.270 Million cell updates/sec

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Perfect score: 1377
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Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Scoring table:
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Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1377	100.0	3082	9	US-09-778-963A-1	Sequence 1, Appli
2	1372	99.6	837	18	US-10-804-491-40	Sequence 40, Appl
3	1372	99.6	2832	10	US-09-918-715-174	Sequence 174, Appl
4	1372	99.6	2832	17	US-10-185-035-4	Sequence 4, Appli
5	1372	99.6	2832	18	US-10-474-794-174	Sequence 174, App
6	1372	99.6	2973	10	US-09-918-715-197	Sequence 197, App
7	1372	99.6	2973	18	US-10-474-794-197	Sequence 197, App
8	1372	99.6	3058	18	US-10-723-860-5134	Sequence 5134, Ap
9	1304	94.7	3020	10	US-09-918-715-292	Sequence 292, App
10	1304	94.7	3020	18	US-10-474-794-292	Sequence 292, Appl
11	911	66.2	11221	9	US-09-778-963A-3	Sequence 3, Appli
12	911	66.2	16000	17	US-10-185-035-11	Sequence 11, Appl
13	911	66.2	114771	18	US-10-027-632-458	Sequence 458, App
14	902	65.5	696	16	US-09-918-386-20951	Sequence 20951, A
15	879	63.8	846	18	US-10-804-491-1	Sequence 1, Appli
16	879	63.8	1740	18	US-10-804-491-45	Sequence 45, Appl
17	879	63.8	1744	14	US-10-197-666A-87	Sequence 87, Appl
18	879	63.8	1801	18	US-10-804-491-3	Sequence 3, Appli
19	586	42.6	1021	17	US-10-321-039-13	Sequence 13, Appl
20	569	41.3	523	18	US-10-185-035-12	Sequence 12, Appl
21	511	37.1	753	13	US-10-027-632-25123	Sequence 25123, A
22	511	37.1	753	13	US-10-027-632-25124	Sequence 25124, A
23	511	37.1	753	13	US-10-027-632-25125	Sequence 25125, A
24	511	37.1	753	17	US-10-027-632-25123	Sequence 25123, A
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26 c	511	37.1	753	17	US-10-027-632-25125	Sequence 25125, A
27 c	464	33.7	368	9	US-09-864-761-21643	Sequence 21643, A
28	373	27.1	405	9	US-09-960-352-10273	Sequence 10273, A
29	344	25.0	1108	15	US-10-037-270-945	Sequence 945, App
30	344	25.0	1108	17	US-10-037-270-945	Sequence 945, App
31	344	25.0	3061	18	US-10-363-829-200	Sequence 200, App
32	344	25.0	4167	18	US-10-399-455-36	Sequence 36, Appl
33 c	343.5	24.9	3440	18	US-10-723-860-8257	Sequence 8257, Ap
34	341	24.8	597	10	US-09-873-546-4	Sequence 4, Appli
35 c	341	24.8	597	16	US-09-918-386-22936	Sequence 22936, A
36	319	23.2	1249	18	US-10-363-829-77	Sequence 77, Appl
37	300	21.8	2223	17	US-10-344-404-22	Sequence 22, Appl
38	297	21.6	1733	16	US-10-996-534-66	Sequence 66, Appl
39	297	21.6	1733	17	US-10-231-956A-428	Sequence 428, App
40	296	21.5	1504	14	US-10-197-666A-81	Sequence 81, Appl
41	296	21.5	2297	18	US-10-322-281-473	Sequence 473, Appl
42	296	21.5	2340	15	US-10-106-698-1073	Sequence 1073, App
43	296	21.5	2624	15	US-10-084-817-186	Sequence 186, App
44	294.5	21.4	3300	15	US-10-037-270-456	Sequence 456, App
45	294.5	21.4	3300	17	US-10-117-722-456	Sequence 456, App

ALIGNMENTS

RESULT 1
US-09-778-963A-1

; Sequence 1, Application US/0977896A
; Patent No. US2002015172A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001112
; CURRENT APPLICATION NUMBER: US/09/778,963A
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 1
; LENGTH: 3082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-963A-1

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; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/804,491
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/09/709,103
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 40
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(834)
; OTHER INFORMATION:
US-10-804-491-40
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Alignment Scores:
Pred. No.:
Score:                  1.8e-168        Length:        837
Percent Similarity:     99.62%          Matches:       265
Best Local Similarity:  99.62%          Conservative:  0
Query Match:            99.64%          Mismatches:    0
DB:                                     Indels:        1
                                        Gaps:          0

US-09-778-963B-2 (1-266) x US-10-804-491-40 (1-837)
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RESULT 2
US-10-804-491-40
; Sequence 40, Application US/10804491
; Publication No. US20040018375A1
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
```

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Alignment Scores:
Pred. No.:
Score:                  3.12e-168       Length:        3082
Percent Similarity:     100.00%         Matches:       266
Best Local Similarity:  100.00%         Conservative:  0
Query Match:            100.00%         Mismatches:    0
DB:                                     Indels:        0
                                        Gaps:          0

US-09-778-963B-2 (1-266) x US-09-778-963A-1 (1-3082)
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Qy    1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
Db  211 ATGATGAAGACTTTGTCCAGCGGGGAACTGCAGCTCAGTGTGCCCGCCAAAAACTCATAC 270

Qy   21 ArgMetValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
Db  271 CGCATGGTGGTGCTGGGTGCCTCTCGGGTGGGGAAGAGCTCCATCGTTGTCTCGCTTCCTC 330

Qy   41 AsnGlyArgPheGluAspGlnIleTyrThrProThrIleGluAspAspPheHisArgGlyLysValTyr 60
Db  331 AATGGGCGCCCTTTGAGGACCAGATACACACCCACCATCGAGGACTTCCACCGTAAGGTATAC 390

Qy   61 AsnIleArgGlyTyrAspMetTyrGlnIleLeuAspIleThrSerGlyAsnHisProPhe 80
Db  391 AACATCCGCGGCCACAGTACCAGCTCGACACATCCCTGATTACCTCTGGCAACCACCCCTTC 450

Qy   81 ProAlaMetArgArgLeuSerIleLeuGluThrGlyAspValPheIleLeuValPheSerLeu 100
Db  451 CCCGCCATGCGCAGGCGTCCATCCTCACAGGGGATGTCTTCATCCTGGTGTTCAGCCTG 510

Qy  101 AspAsnArgGluSerPheAspGluValLeuValLysArgLeuGlnIleLeuGluGluLys 120
Db  511 GATAACCGGGAGTCTTCGATGAGGTCAAGGTCCTGGTGGTTCAAG 570

Qy  121 SerCysLeuLysValSerAsnLysThrLysGlnAlaAlaGluLeuProMetValIleIleCysGlyAsn 140
Db  571 TCCTGCCTGAAGAACAAGACCAAGGAGGGGCGGGAGCTGCCCATGGTCATCTGTGGCAAC 630

Qy  141 LysAsnAspHisGlyLysGlnValProLeuThrThrGlyIleAlaGluLeuLeuLeuVal 160
Db  631 AAGAACGACCACGGCCAGGGCCTGCCCCAGTGCCACCGAGGCCGGAGCTGCTGGTG 690

Qy  161 SerGlyAspProGluAsnSerAlaTyrPheGluValLeuSerAlaLysAsnThrAsnValAsp 180
Db  691 TCGGGCGACCCGGAGAACTCCGCCTACTTCGAGGTGCTGGCCAAGAACACCAACGTGGAC 750

Qy  181 GluMetPheTyrValLeuProHisGlnMetSerProAlaLeu 200
Db  751 GAGATGTTCTACGTGCTGCCTCACCAGATGAGCCCCGCCCTG 810

Qy  201 HisArgLysIleSerValGlnThrGlyAspAlaPheHisGluLeuProHisGluLysAspAsn 220
Db  811 CATCGCAAGATCTCCGTGCAGACTGGCGGCCCTTCGATGTGAC 870

Qy  221 ArgValLysGluMetAspAlaTyrGlyMetValSerProPheAlaArgArgProSerVal 240
Db  871 CGGGTCAAGGAGATGGACGCCTATGGCATGGTCTCGCCCTTCGCCCGCCGCCCAGCGGTC 930

Qy  241 AsnSerAspLeuLysTyrIleLysAlaLysValLeuArgGluLysGlnLysAlaArgGluArg 260
Db  931 AACAGCGACCTGAAGTACATCAAGGCCAAGGTCCTGCGGGAAAGGCCAGCGCCGTGAGAGG 990

Qy  261 AspGlyLysCysGlyThrIleGln 266
Db  991 GACAGAGTGCACCATCCAG 1008
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Db   697 CGCGTCAAGGAGGATGGAGCCCTATGGCATGGGTCTCGCCCGCCCTTCGCCGCCGGGTC 756
Qy   241 AsnSerAspLeuLysTyrIleLysValLeuArgGluGlyGlnAlaArgGluArg 260
Db   757 AACAGTGACCCTCAAGTACATCAAGGCCCAAGGTCCTTCGGGAGGGCCCCGTGAGAGG 816
Qy   261 AspLysCysThrIleGln 266
Db   817 GACAAGTGCACCATCCAG 834

RESULT 3
US-09-918-715-174
Sequence 174, Application US/0991871S
Publication No. US2003017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 2832
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-174

Alignment Scores:
Pred. No.:
Score: 1372.00
Percent Similarity: 99.62%
Best Local Similarity: 99.62%
Query Match: 99.64%
DB: 10

			Length: 2832
			Matches: 265
			Conservative: 0
			Mismatches: 1
			Indels: 0
			Gaps: 0

US-09-778-963B-2 (1-266) x US-09-918-715-174 (1-2832)

Qy   1   MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
Db   37   ATGATGAAGACTTTGTCCAGCGGGAACTGCACGCTCAGTGTGCCCGCAAAAAACTCATAC 96

Qy   21   ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
Db   97   CGCATGGTGGTTCTGGGTGCCTCTCGGGTGGGCAAGAGCTCCATCGTGTCTCGGTTCCTC 156

Qy   41   AsnGlyArgPheGluAspGlnThrTyrThrProThrIleGluAspPheHisArgGlyValTyr 60
Db   157 AATGGCCGCTTTGAGGACCAGACGTACACACCCACCATCGAGGACTTCCACCGTAAGGTATAC 216

Qy   61   AsnIleArgGlyAspMetTyrGlnLeuLeuAspThrSerGlyGlyAsnHisProPhe 80
Db   217 AACATCCGCGGCGACATGTACCAGCTGCGATACTCTGGATACTCTGGAGGCAACCACCCCTTC 276

Qy   81   ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
Db   277 CCCGCCATGCGCAGGCTGTCCATCCTCACAGGGAGTGTCTTCATCCTGGTGTTCAGCCTG 336

Qy   101 AspAspAlaArgGluSerPheAspGluValArgArgLeuGlnIleIleLeuGluValLys 120
Db   337 GATGATGCCCGGGAGTCCTTCGATGAGGTCAGGCGCTTCAGGAGCAGATCCTGGAGGTCAAG 396

Qy   121 SerCysLeuLysAsnLysThrLysGluAlaAlaGlyLeuProMetValIleCysGlyAsn 140

Db   397 TCCTGCCTGAGGAACAAGACAAGAGGAGGCCAAGGAGCGGGGGGAGGAGCTGCCCATGGTGATCTGTGGCAAC 456
Qy   141 LysAsnAspHisGlyGluLeuCysSerArgGlnValProThrThrGluAlaGluLeuLeuVal 160
Db   457 AAGAACGACCACGGCGAGCTGTGCCGCAGGGTGCCCACCACGGAGGCCGAGCTGCTGGTG 516
Qy   161 SerGlyAspGluValAsnSerAlaTyrPheGluValSerAlaLysAsnThrAsnValAsp 180
Db   517 TCGGGCGACGAGGTGAACTCGGCCTACTTCGAGGTGTCGGCCAAGAACACCAACGTGGAC 576
Qy   181 GluMetPheTyrValLeuPheSerMetAlaLysGluLeuProHisGluMetSerProAlaLeu 200
Db   577 GAGATGTTCTACGTGCTCTTCAGCATGGCCAAGGCTGCCACACGAGATGAGCCCGCCCTG 636
Qy   201 HisArgLysIleSerValGlnThrArgGlyAspAlaPheHisAspArgProPheCysMetArg 220
Db   637 CATCGCAAGATCTCCGTGCAGTACCGGGTGGACGCCTTCCACCCCAGGCCGTTCTGCATGCGC 696
Qy   221 ArgValGlyGluMetAspAlaTyrGlyMetValSerProPheAlaArgGlyArgProSerVal 240
Db   697 CGCGTCAAGGAGGATGGAGCCCTATGGCATGGGTCTCGCCCGCCCTTCGCCGCCGGGTC 756
Qy   241 AsnSerAspLeuLysTyrIleLysValLeuArgGluGlyGlnAlaArgGluArg 260
Db   757 AACAGTGACCCTCAAGTACATCAAGGCCCAAGGTCCTTCGGGAGGGCCCCGTGAGAGG 816
Qy   261 AspLysCysThrIleGln 266
Db   817 GACAAGTGCACCATCCAG 834

RESULT 4
US-10-185-035-4
Sequence 4, Application US/10185035
Publication No. US20040005706A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DEXRAS1 EXPRESSION
; FILE REFERENCE: RTS-0377
; CURRENT APPLICATION NUMBER: US/10/185,035
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 4
; LENGTH: 2832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(837)
US-10-185-035-4

Alignment Scores:
Pred. No.:
Score: 1372.00
Percent Similarity: 99.62%
Best Local Similarity: 99.62%
Query Match: 99.64%
DB: 17

			Length: 2832
			Matches: 265
			Conservative: 0
			Mismatches: 1
			Indels: 0
			Gaps: 0

US-09-778-963B-2 (1-266) x US-10-185-035-4 (1-2832)

Qy   1   MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
Db   37   ATGATGAAGACTTTGTCCAGCGGGAACTGCACGCTCAGTGTGCCCGCAAAAAACTCATAC 96

Qy   21   ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
Db   97   CGCATGGTGGTTCTGGGTGCCTCTCGGGTGGGCAAGAGCTCCATCGTGTCTCGGTTCCTC 156

Qy   41   AsnGlyArgPheGluAspGlnThrTyrThrProThrIleGluAspPheHisArgGlyValTyr 60
Db   157 AATGGCCGCTTTGAGGACCAGACGTACACACCCACCATCGAGGACTTCCACCGTAAGGTATAC 216

Left column (RESULT 5)

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Alignment Scores:
Pred. No.:             1.23e-167            Length:        2832
Score:                 1372.00              Matches:       265
Percent Similarity:    99.62%               Conservative:  0
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US-10-474-794-174
;  ORGANISM: Homo sapiens
;  TYPE: DNA
;  LENGTH: 2832
;  SEQ ID NO 174
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  NUMBER OF SEQ ID NOS: 359
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/308,829
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: 60/282,850
;  CURRENT FILING DATE: 2003-10-14
;  CURRENT APPLICATION NUMBER: US/10/474,794
;  FILE REFERENCE: 1107.00179
;  TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
;  APPLICANT: Kinzler, Kenneth
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: St. Croix, Brad
;  APPLICANT: Carson-Walter, Eleanor
;  GENERAL INFORMATION:
;  Publication No. US20040213793A1
;  Sequence 174, Application US/10474794
US-10-474-794-174
RESULT 5
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Qy    61  AsnIleArgGlyAspMetTyrGlnLeuAspThrSerGlyAsnHisProPhe   80
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   217  AACATCCGCGGCGACATGTACCAGCTCGACACTTCAGGCAACCACCCCTTC  276

Qy    81  ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerIleLeu  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   277  CCCGCCATGCGCAGGCTGTCCATCCTCACAGGGGATGTCTTCATCCTGGTGTTCAGCCTG  336

Qy   101  AspAlaAsnArgGluSerProheAspGluValLysArgGlnLysGlnIleLeuGluGlyValLys  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   337  GATGCCAACCGGGAGTCCTTCGATGAGGTCAAGCGCCTTCAGAGACAGAATCCTCAAG  396

Qy   121  SerCysLeuLysGlyLysAsnLysValThrLysLysLeuValAlaLeuAlaGlyLeuProMetValIleLeuCysGlyAsn  140
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397  TCCTGCCTGAAGAACAAGAAGGAGGCGGAGCTGCCCATGGTCATCCTGTGTGGCAAC  456

Qy   141  LysAsnAspHisHisGlyGlyLeuCysArgGlnValProThrThrGluAlaGluLeuLeuLeuVal  160
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   457  AAGAACGACCACCACGGCGGACTGTGCCGCCAGGTCCCCACCACCGAGGCTGAGCTGCTGGTG  516

Qy   161  SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaLysLysLysAsnThrAsnValAsp  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   517  TCGGGCGACGAGAACTCGGCCTACTTCGAGGTGTCGGCCAAGAAGAACACCAACGTGGAC  576

Qy   181  GluMetPheTyrValLeuPheSerMetAlaLysLysProHisGluMetSerProAlaLeu  200
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   577  GAGATGTTCTACGTGCTCTTCAGCATGGCCAAGCTGCCCACACGGATGAGCCCGCCCTG  636

Qy   201  HisArgLysIleSerValGlnIleTyrGlyAspAlaPheHisProArgProPheCysMetArg  220
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   637  CATCGCAAGATCTCCGTGCAGATCTACGGTGACGCCTTCCACCCCAGGCCCTTCTGCATGCGC  696

Qy   221  ArgValLysGluLeuMetAspAlaThrArgGlyMetValSerProPheAlaArgArgProSerVal  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   697  CGCGTCAAGGAGCTGATGGACGCCTATCGGGGCATGGTCTCGCCCTTCGCCCGCCGCCCCAGCGTC  756

Qy   241  AsnSerAsnLeuLysLysTyrIleLeuLysSerAlaLeuValLeuLysArgGlnGlnAlaArgGluArg  260
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   757  AACAGTAACCTCAAGAAGTACATCAAGGCCAAGGTCCTTCGGGAGGGCCAAGGCCCGTGAGAGG  816

Qy   261  AspLysCysThrIleGln  266
          ||||||||||
Db   817  GACAAGTGCACCATCCAG  834
```

Right column

```
US-09-778-963B-2 (1-266)  x  US-10-474-794-174 (1-2832)

Best Local Similarity:   99.62%           Mismatches:  1
Query Match:             99.64%           Indels:      0
DB:                      18               Gaps:        0
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```
Qy     1  MetMetLeuThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr  20
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    37  ATGATGAACGACTTTGTCCACGGGGAACTGCACGCTCAGTGTGCCCGGAAAAACTCATAC  96

Qy    21  ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu  40
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    97  CGCATGGTGGTGCTGGGTGCCTCCCGGGTGGGCAAGAGCTCCATCGTGTCTCGCTTCCTC  156

Qy    41  AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   157  AATGGCCGCTTTGAGGACCAGTACACACCCACCATCGAGGACTTCCACCGTAAGGTATAC  216

Qy    61  AsnIleArgGlyAspMetTyrGlnLeuAspThrSerGlyAsnHisProPhe  80
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   217  AACATCCGCGGCGACATGTACCAGCTCGACACTTCAGGCAACCACCCCTTC  276

Qy    81  ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerIleLeu  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   277  CCCGCCATGCGCAGGCTGTCCATCCTCACAGGGGATGTCTTCATCCTGGTGTTCAGCCTG  336

Qy   101  AspAlaAsnArgGluSerProheAspGluValLysArgGlnLysGlnIleLeuGluGlyValLys  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   337  GATGCCAACCGGGAGTCCTTCGATGAGGTCAAGCGCCTTCAGAGACAGAATCCTCAAG  396

Qy   121  SerCysLeuLysGlyLysAsnLysValThrLysLysLeuValAlaLeuAlaGlyLeuProMetValIleLeuCysGlyAsn  140
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397  TCCTGCCTGAAGAACAAGAAGGAGGCGGAGCTGCCCATGGTCATCCTGTGTGGCAAC  456

Qy   141  LysAsnAspHisHisGlyGlyLeuCysArgGlnValProThrThrGluAlaGluLeuLeuLeuVal  160
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   457  AAGAACGACCACCACGGCGGACTGTGCCGCCAGGTCCCCACCACCGAGGCTGAGCTGCTGGTG  516

Qy   161  SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaLysLysLysAsnThrAsnValAsp  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   517  TCGGGCGACGAGAACTCGGCCTACTTCGAGGTGTCGGCCAAGAAGAACACCAACGTGGAC  576

Qy   181  GluMetPheTyrValLeuPheSerMetAlaLysLysProHisGluMetSerProAlaLeu  200
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   577  GAGATGTTCTACGTGCTCTTCAGCATGGCCAAGCTGCCCACACGGATGAGCCCGCCCTG  636

Qy   201  HisArgLysIleSerValGlnIleTyrGlyAspAlaPheHisProArgProPheCysMetArg  220
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   637  CATCGCAAGATCTCCGTGCAGATCTACGGTGACGCCTTCCACCCCAGGCCCTTCTGCATGCGC  696

Qy   221  ArgValLysGluLeuMetAspAlaThrArgGlyMetValSerProPheAlaArgArgProSerVal  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   697  CGCGTCAAGGAGCTGATGGACGCCTATCGGGGCATGGTCTCGCCCTTCGCCCGCCGCCCCAGCGTC  756

Qy   241  AsnSerAsnLeuLysLysTyrIleLeuLysSerAlaLeuValLeuLysArgGlnGlnAlaArgGluArg  260
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   757  AACAGTAACCTCAAGAAGTACATCAAGGCCAAGGTCCTTCGGGAGGGCCAAGGCCCGTGAGAGG  816

Qy   261  AspLysCysThrIleGln  266
          ||||||||||
Db   817  GACAAGTGCACCATCCAG  834
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```
RESULT 6
US-09-918-715-197
;  Sequence 197, Application US/0918715
;  Publication No. US20030017157A1
;  GENERAL INFORMATION:
;  APPLICANT: Brad St. Croix
;  APPLICANT: Bert Vogelstein
;  APPLICANT: Kenneth Kinzler
;  TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
;  FILE REFERENCE: 1107.00134
;  CURRENT APPLICATION NUMBER: US/09/918,715
```

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; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SEQ ID NO 197
; LENGTH: 2973
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-197

Alignment Scores:
Pred. No.:                  1.32e-167
Score:                      1372.00        Length:        2973
Percent Similarity:         99.62%         Matches:       265
Best Local Similarity:      99.62%         Conservative:  0
Query Match:                99.64%         Mismatches:    1
DB:                         10             Indels:        0
                                           Gaps:          0

US-09-778-963B-2 (1-266) x US-09-918-715-197 (1-2973)

Qy       1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 ATGATGAAGACTTTGTCCAGCGGGGAACTGCACGGCTCAGTGTCGCCCGCCAAAAACTCATAC 267

Qy      21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 CGCATGGTGGTGCTTGGGGTGCCTCGGGTGGGCAAGAGCTCCATCGTGTCTCGCTTCCTC 327

Qy      41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 AATGGCCGCTTTGAGGACCAGTACACACCCACCATCGAAGACTTCCACCGTAAGGTTATAC 387

Qy      61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 AACATCCGCGGCGACATGTACCAGCTCGACATCCTGGATACCTCTGGCAAC 447

Qy      81 ProAlaMetArgArgLeuThrGlyAspValPheIleLeuValPheSerLeu 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 CCCGCCATGCGCAGGCTGTCCATCCTCACAGGGGATGTCTTCATCCTGGTGTTCAGCCTG 507

Qy     101 AspAsnArgGluSerPheAspGluValLysArgLeuGlnIleLeuGluVallys 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     508 GATAACCGGGAGTCCTTCGATGAGGTCAAGCGCCCTTCAGAGCAGATCCCTGGAGGTCAAG 567

Qy     121 SerCysGlyLeuLysAsnLysThrLysGluAlaAlaGluLeuProMetValIleCysGlyAsn 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 TCCTGCCTGAAGAACAAGACAAAGGAGGCGGCTGAGCTGCCCATGGTCATCTGTGGCAAC 627

Qy     141 LysAsnAspHisGlyGlyLeuCysArgGlnValProThrThrGluAlaGluLeuLeuVal 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 AAGAACGACCACGGCGGACTGTGCCGCCAGGTGCCCACCACCGAGGCCGAGCTGCTGGTG 687

Qy     161 SerGlyLysAspGluAsnSerAlaTyrPheGluValSerAlaLysGlyAsnThrAsnValAsp 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 TCGGGCAAGGACGAGAACTCGGCCTACTTCGAGGTGTCGGCCAAAGGAAACACCAACGTGGAC 747

Qy     181 GluMetPheTyrValGlnMetSerMetAlaLysGluMetSerProAlaLeu 200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 GAGATGTTCTACGTGCTTCAGCATGGCCAAGCTGGCCCACAGCGATGAGCCCCCGCCCTG 807

Qy     201 HisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProCysMetArg 220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     808 CATCGCAAGATCTCCGTGCAGTACGGTGACGGCCTTCCACCCAGGCCCTTGCATGCGC 867

Qy     221 ArgValLysGluMetAspAlaTyrGlyMetValSerProPheAlaArgArgProSerVal 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     868 CGGGTCAAGGAGATGGATGCCTATGGCATGGTCTCGCCCTTTGCCCGCCGGCCCAGCGTC 927
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```
; CURRENT FILING DATE: 2001-08-01
RESULT 7
US-10-474-794-197
; Sequence 197, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
;  APPLICANT: Carson-Walter, Eleanor
;  APPLICANT: St. Croix, Brad
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth
;  TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
;  FILE REFERENCE: 1107.00179
;  CURRENT APPLICATION NUMBER: US/10/474,794
;  CURRENT FILING DATE: 2003-10-14
;  PRIOR APPLICATION NUMBER: 60/282,850
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: 60/308,829
;  PRIOR FILING DATE: 2001-08-01
;  NUMBER OF SEQ ID NOS: 359
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 197
;  LENGTH: 2973
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-474-794-197

Alignment Scores:
Pred. No.:                  1.32e-167
Score:                      1372.00        Length:        2973
Percent Similarity:         99.62%         Matches:       265
Best Local Similarity:      99.62%         Conservative:  0
Query Match:                99.64%         Mismatches:    1
DB:                         18             Indels:        0
                                           Gaps:          0

US-09-778-963B-2 (1-266) x US-10-474-794-197 (1-2973)

Qy       1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 ATGATGAAGACTTTGTCCAGCGGGGAACTGCACGGCTCAGTGTCGCCCGCCAAAAACTCATAC 267

Qy      21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 CGCATGGTGGTGCTTGGGGTGCCTCGGGTGGGCAAGAGCTCCATCGTGTCTCGCTTCCTC 327

Qy      41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 AATGGCCGCTTTGAGGACCAGTACACACCCACCATCGAAGACTTCCACCGTAAGGTTATAC 387

Qy      61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 AACATCCGCGGCGACATGTACCAGCTCGACATCCTGGATACCTCTGGCAAC 447

Qy      81 ProAlaMetArgArgLeuThrGlyAspValPheIleLeuValPheSerLeu 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 CCCGCCATGCGCAGGCTGTCCATCCTCACAGGGGATGTCTTCATCCTGGTGTTCAGCCTG 507

Qy     101 AspAsnArgGluSerPheAspGluValLysArgLeuGlnIleLeuGluVallys 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     508 GATAACCGGGAGTCCTTCGATGAGGTCAAGCGCCCTTCAGAGCAGATCCCTGGAGGTCAAG 567

Qy     121 SerCysGlyLeuLysAsnLysThrLysGluAlaAlaGluLeuProMetValIleCysGlyAsn 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 TCCTGCCTGAAGAACAAGACAAAGGAGGCGGCTGAGCTGCCCATGGTCATCTGTGGCAAC 627

Qy      61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 AACATCCGCGGCGACATGTACCAGCTCGACATCCTGGATACCTCTGGCAAC 387

Qy     141 LysAsnAspHisGlyGlyLeuCysArgGlnValProThrThrGluAlaGluLeuLeuVal 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy     241 AsnSerArgAspLeuLysThrIleLysLeuAsnAlaLysValLeuArgGluGlnGlnAlaArgGluArg 260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     928 AACAGTGACCTCAAGTACATCAAGCTCAATGCCAAGGTCCTTCGGGAGAAGGCCAGGGCCCGTGAGAGG 987

Qy     261 AspLysCysThrIleGln 266
           |||||||||||||||||||
Db     988 GACAAGTGCACCATCCAG 1005
```

Qy 628 AAGAACGACCACCGCGACGCTGTCCGCCACCGAGGTGCCCACCGAGGCCGAGCTGCTGGTG 687
Db 688 TCCGGCGACGAGAACTGCGCCCTACTTCAGGTGTCGGCGGAGAAGACACCAACGTGGAC 747

Qy 161 SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaLysLysAsnThrAsnValAsp 180
Db 688 TCCGGCGACGAGAACTGCGCCCTACTTCAGGTGTCGGCGGAGAAGACACCAACGTGGAC 747

Qy 181 GluMetPheTyrValLeuPheSerMetAlaLysLeuProHisGluMetSerProAlaLeu 200
Db 748 GAGATGTTCTACGTGCTCTTCAGCATGGCCAAGCTGCCACACGAGATGAGCCCGCCCTG 807

Qy 201 HisArgLysIleSerValGlnThrTyrGlyAspAlaPheHisProArgProPheCysMetArg 220
Db 808 CATCGCAAGATCTCCGTGCAGACGTACGGGGACGCCTTCCACCCCAGGCCCTTCTGCATGCGC 867

Qy 221 ArgValLysGluMetAspAlaTyrGlyMetValSerProPheAlaAlaArgProSerVal 240
Db 868 CGCGTCAAGGAGATGGACGCGTATGGCATGGTGTCCCCGTTCGCCGCCCGGCCCAGCGTC 927

Qy 241 AsnSerAspLeuLysTyrIleLeuLysAlaLysAlaValLeuLeuArgGlyHisGlnAlaArgGluArg 260
Db 928 AACAGTGACCTCAAGTACATCAAGGCCAAGGCCGTCCTTCGGGGAAGGCCAGGCCCGTGAGAGG 987

Qy 261 AspLysCysThrIleGln 266
Db 988 GACAAGTGCACCATCCAG 1005

RESULT 8

US-10-723-860-5134
Sequence 5134, Application US/10723860
Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SEQ ID NO 5134
; LENGTH: 3058
; TYPE: DNA
; ORGANISM: Homo sapiens
; SOFTWARE: Patentin version 3.2

Alignment Scores:
Pred. No.:
Score: 1372.00
Percent Similarity: 99.62%
Best Local Similarity: 99.62%
Query Match: 99.64%
DB:

US-10-723-860-5134
LENGTH: 3058

US-09-778-963B-2 (1-266) x US-10-723-860-5134 (1-3058)

Length: 3058
Matches: 265
Conservative: 1
Mismatches: 0
Indels: 0
Gaps: 0

Qy   1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
Db 217 ATGATGAAGACTTTGTCCAGCGGGAACTGCACGCTCAGTGTGCCCGCAAAAAACTCATAC 276

Qy   21 ArgMetValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
Db 277 CGCATGGTGGTGCTCGGGGTGGGCAAGAGCTCCATCGTGTCTCGCTTCCTC 336

Qy   41 AsnGlyArgPheGluAspProGlnThrTyrThrProThrIleGluAspPheHisArgLysValTyr 60
Db 337 AATGGCCGCTTTGAGGACCCAGTACACACCACCCACCATCGAGGACTTCCACCGTAAGGTATAC 396

Qy   61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80

Db 397 AACATCCGCGGGGACATGTACCAGCTCGACATCCTGGATACCTCTGGCAACCACCCCTTC 456
Qy   81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuLeuValPheSerLeu 100
Db 457 CCCGCAATGCGCAGGCTGTCCATCCTCACAGGGGATGTCTTCATCCTGCTGGTGTTCAGCCTG 516

Qy 101 AspAsnArgGluSerPheAspGluValLysArgLeuGlnLysGlnIleLeuGluGluVal 120
Db 517 GATAACCGGGAGAGCTTCGATGAGGTCAAGAGGCTGCAGAAGCAGATCCTGGAGGTCAAG 576

Qy 121 SerCysLeuLysTyrThrLysGluAlaAlaLeuProMetValIleCysGlyAsn 140
Db 577 TCCTGCCTCAAGTACACCAAGGAGGCGGCGCTGCCCATGGTCATCTGTGGCAAC 636

Qy 141 LysAsnAspLysSerGlyValGlnValProThrThrGluValLeuLeuLeuVal 160
Db 637 AAGAACGACAAGAGCGGGGTGCAGGTGCCCACCACAGAGGTGCTGCTGGTG 696

Qy 161 SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaLysLysAsnThrAsnValAsp 180
Db 697 TCCGGCGACGAGAACTCGCCCTACTTCGAGGTGTCGGCCAAGAAGAACACCAACGTGGAC 756

Qy 181 GluMetPheTyrValLeuPheSerMetAlaLysLeuProHisGluMetSerProAlaLeu 200
Db 757 GAGATGTTCTACGTGCTCTTCAGCATGGCCAAGCTGCCACACGAGATGAGCCCGCCCTG 816

Qy 201 HisArgLysIleSerValGlnThrTyrGlyAspAlaPheHisProArgProPheCysMetArg 220
Db 817 CATCGGAAGATCTCCGTGCAGACGTACGGGGACGCCTTCCACCCCAGGCCCTTCTGCATGCGC 876

Qy 221 ArgValLysGluMetAspAlaTyrGlyMetValSerProPheAlaAlaArgProSerVal 240
Db 877 CGCGTCAAGGAGATGGACGCGTATGGCATGGTGTCCCCGTTCGCCGCCCGGCCCAGCGTC 936

Qy 241 AsnSerAspLeuLysTyrIleLeuLysAlaLysAlaValLeuLeuArgGlyHisGlnAlaArg 260
Db 937 AACAGTGACCTCAAGTACATCAAGGCCAAGGCCGTCCTTCGGGGAAGGCCAGGCCCGTGAGAGG 996

Qy 261 AspLysCysThrIleGln 266
Db 997 GACAAGTGCACCATCCAG 1014

RESULT 9

US-09-918-715-292
Sequence 292, Application US/09918715
Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Kenneth Kinzler
; APPLICANT: Bert Vogelstein
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 292
; LENGTH: 3020
; TYPE: DNA
; ORGANISM: Mouse
US-09-918-715-292

Alignment Scores:
Pred. No.:
Score: 1304.00
Percent Similarity: 96.24%
Best Local Similarity: 94.74%

Length: 3020
Matches: 252
Conservative: 4
Mismatches: 10

```
;  CURRENT APPLICATION NUMBER: US/10/474,794
;  FILE REFERENCE: 1107.0179
;  TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
;  APPLICANT: Kinzler, Kenneth
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: St. Croix, Brad
;  APPLICANT: Carson-Walter, Eleanor
;  GENERAL INFORMATION:
;  Publication No. US20040213793A1
;  Sequence 292, Application US/10474794
RESULT 10
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;  CURRENT FILING DATE: 2003-10-14
;  PRIOR APPLICATION NUMBER: 60/282,850
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: 60/308,829
;  PRIOR FILING DATE: 2001-08-01
;  NUMBER OF SEQ ID NOS: 359
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 292
;  LENGTH: 3020
;  TYPE: DNA
;  ORGANISM: Mouse
DB:  US-10-474-794-292
```

US-09-778-963B-2 (1-266) x US-10-474-794-292 (1-3020)

```
Alignment Scores:
Pred. No.:
Score:                  1.02e-158          Length:        3020
Percent Similarity:     1304.00            Matches:       252
Best Local Similarity:  96.24%             Conservative:  4
Query Match:            94.74%             Mismatches:    10
                        94.70%             Indels:        0
                                           Gaps:          0
Query Match:  18
```

Query Match: 94.70%   Indels: 0
DB: 10   Gaps: 0

US-09-778-963B-2 (1-266) x US-09-918-715-292 (1-3020)

```
Qy    1  MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr   20
         ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db  376  ATGATGAAGACCTTGTCCAGTGGGAACTGCACACTCAATGTGCCTGTAAGAAACTCCTAC  435

Qy   21  ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu   40
Db  436  CGCATGGTGGTCCTGGGTGCCTCCCGAGTGGGCAAGAGCTCCATTGTCTCCCGGCTTCTC  495

Qy   41  AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr   60
Db  496  AATGGCCGCTTTGAGGACCAGTACACCCCCACTATCGAAGACTTTCACCGAAAGGTGTAC  555

Qy   61  AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe   80
Db  556  AACATCCGAGGGGACATGTACCAGCTGGATATCCTGGACACTTCTGGCAACCACCCATTC  615

Qy   81  ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu  100
Db  616  CCTGCCATGCGCCGGCTCTCCATCCTCACAGGAGATGTCTTCATCCTGGTGTTCAGCCTG  675

Qy  101  AspAsnArgGluSerPheAspGluValValLysAspLeuGlnAsnIleLeuGluValLys  120
Db  676  GATAGCCGGGAGAGTTCCTTTGATGAGGTCGTAAAGGACCTTCAGAACATCCTGGAAGTC  735

Qy  121  SerCysSerLeuLysAsnLysThrLysGlyLeuAlaLeuAlaLeuGluLeuProMetVal  140
Db  736  TCCTGCTCACTGAAGAATAAAACCAAGGGACTGGCTCTGGCTCTGGAACTG  795

Qy  141  LysAsnAspHisGlyGlyLeuGluLeuGlnValProThrThrGlnGlyLeuLeuLeuVal  160
Db  796  AAGAATGACCACGGTGGCTGTGCCCTGGAGCTGCAGGTGGTG  855

Qy  161  SerGlyAspAsnSerAlaTyrPheGluValLysSerAlaLysValLysAsnThrAsnVal  180
Db  856  TCTGGTGATAACAGCGCCTATTTCGAGGTGTCAGCCAAGAGAACACTAAATGTGAAC  915

Qy  181  GluMetPheTyrValLeuPheSerMetAlaLysLeuGluProHisGluMetSerProAla  200
Db  916  GAGATGTTCTATGTGCTGTTCAGCATGGCCAAGCTGGAGCCCCATGAGATGAGCCCTGCA  975

Qy  201  HisArgLysIleSerGlyValGlnTyrGlyAspAlaPheHisProArgProPheCysMetArg  220
Db  976  CACCATAAGATCTCCGGTGCAGTACGGGCGATGCTTTTCACCCCGCC  1035

Qy  221  ArgValLysGluMetAspAlaTyrGlyMetValSerProPheAlaArgAlaArgProSerVal  240
Db 1036  CGCACTAAGGTCGCAGGTGCCTATGGCATGGTCTCACCCTTTGCCCGAGC  1095

Qy  241  AsnSerAspLeuLysTyrIleLysAlaLysValLeuArgGlyLysGlyGlnAlaArgGlyArg  260
Db 1096  AACAGTGACCTCAAGTACATCAAGGCCAAGGTCCTACGGGAGGGCCAGGCCCGAGAGAGG  1155

Qy  261  AspGlyLysCysThrIleGln  266
Db 1156  GACAAGTGTAGCATCCAG  1173
```

Db   1096 AACAGTGACCTCAAGTACATCAAGGCCAAGGTCCTACGGGAGGGCCAGGCCCGAGAGAG 1155
          |||||||||||||||||||||||:::||||||
Qy   261 AspLysCysThrIleGln 266
Db   1156 GACAAGTGTAGCATCCAG 1173

RESULT 11

US-09-778-963A-3
; Sequence 3, Application US/09778963A
; Patent No. US2002015172A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001112
; CURRENT APPLICATION NUMBER: US/09/778,963A
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11221
; TYPE: DNA
; ORGANISM: Homo sapiens
DB: US-09-778-963A-3

Alignment Scores:
Pred. No.:
Score: 1.56e-106   Length: 11221
                         911.00   Matches: 176
Percent Similarity: 98.33%   Conservative: 1
Best Local Similarity: 97.78%   Mismatches: 3
Query Match: 66.16%   Indels: 0
DB: 9   Gaps: 0

US-09-778-963A-3 (1-266) x US-09-778-963A-3 (1-11221)

Qy   87 SerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgGluSerPhe 106
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7681 TCTCTCCCTCGCAGGGGATGTCTTCATCCTGGTTGTTCAGCCTGGATAACCGGGAGTCCTTC 7740

Qy   107 AspGluValLysArgLeuGlnLysGlyIleLeuLeuGluGluValValSerGlyAsnLys 126
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7741 GATGAGGTTAAACGCCTTCAGAAGGCAGGATCCTTGGAGGTTGAGGTCGTAAGTGGGAACAAG 7800

Qy   127 ThrLysGluAlaAlaGluLeuProMetValIleCysGlyAsnLysAsnAspHisGlyGlu 146
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7801 ACCAAGGAGGCGGCGGAGCTGCCCATGGTCATCTGTGGCAACAAGAACGACCACGGCGAG 7860

Qy   147 LeuCysArgGlnValProThrThrArgGluAlaGluLeuLeuValSerGlyAspGluAsnSer 166
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7861 CTGTGCCGCCAGGTGCCCACCACCAGGGAAGCTGCTCGGTTGTCCGGGACGAGAACTGC 7920

Qy   167 AlaTyrPheGluValSerAlaLysAlaLysAspGluAsnThrAsnValAspGluMetPheTyrValLeu 186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7921 GCCTACTTCGAGGTGTCGGCCAAGAGAAACACCAACGTGGACGAGATGTTCTACGTGCTC 7980

Qy   187 PheSerMetAlaAlaLysLeuProHisGluMetSerProAlaLeuHisArgLysIleSerVal 206
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 7981 TTCAGCATGGCCAAGCTGCCACACGAGATGAGCCCCGCCCTGCATCGCAAGATCTCCGTG 8040

Qy   207 GlnThrTyrGlyAspAlaPheHisProArgProPheCysMetArgArgValLysGluMetAsp 226
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8041 CAGTACGGGTGACGCGCCTTCCACCCAAGGCCCTTCTGCATGCGGCCGCGTCAAGGAGATGGAC 8100

Qy   227 AlaTyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyr 246
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8101 GCCTATGGCATGGTCTCGCCCTTCGCCCGCCGGCCCTCAGCAGTGAACAGTGACCTCAAGTAC 8160

Qy   247 IleLysAlaLysValLeuArgGluGlyGlnAlaArgGluAspLysCysThrIleGln 266
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8161 ATCAAGGCCAAGGTCCTTCGGGAAGGCCAGGCCCGTGAGAGGGACAAGTGCACCATCCAG 8220

RESULT 12

US-10-185-035-11
; Sequence 11, Application US/10185035
; Publication No. US20040005706A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF DEXRAS1 EXPRESSION
; FILE REFERENCE: RTS-0377
; CURRENT APPLICATION NUMBER: US/10/185,035
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 11
; LENGTH: 16000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-185-035-11

Alignment Scores:
Pred. No.:
Score: 2.73e-106   Length: 16000
                         911.00   Matches: 176
Percent Similarity: 98.33%   Conservative: 1
Best Local Similarity: 97.78%   Mismatches: 3
Query Match: 66.16%   Indels: 0
DB: 17   Gaps: 0

US-09-778-963B-2 (1-266) x US-10-185-035-11 (1-16000)

Qy   87 SerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgGluSerPhe 106
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11913 TCTCTCCCTCGCAGGGGATGTCTTCATCCTGGTTGTTCAGCCTGGATAACCGGGAGTCCTTC 11972

Qy   107 AspGluValLysArgLeuGlnLysGlyIleLeuLeuGluGluValValSerGlyAsnLys 126
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11973 GATGAGGTTAAACGCCTTCAGAAGGCAGGATCCTTGGAGGTTGAGGTCGTAAGTGGGAACAAG 12032

Qy   127 ThrLysGluAlaAlaGluLeuProMetValIleCysGlyAsnLysAsnAspHisGlyGlu 146
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12033 ACCAAGGAGGCGGCGGAGCTGCCCATGGTCATCTGTGGCAACAAGAACGACCACGGCGAG 12092

Qy   147 LeuCysArgGlnValProThrThrArgGluAlaGluLeuLeuValSerGlyAspGluAsnSer 166
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12093 CTGTGCCGCCAGGTGCCCACCACCAGGGAAGCTGCTCGGTTGTCCGGGACGAGAACTGC 12152

Qy   167 AlaTyrPheGluValSerAlaLysAlaLysAspGluAsnThrAsnValAspGluMetPheTyrValLeu 186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12153 GCCTACTTCGAGGTGTCGGCCAAGAGAAACACCAACGTGGACGAGATGTTCTACGTGCTC 12212

Qy   187 PheSerMetAlaAlaLysLeuProHisGluMetSerProAlaLeuHisArgLysIleSerVal 206
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12213 TTCAGCATGGCCAAGCTGCCACACGAGATGAGCCCCGCCCTGCATCGCAAGATCTCCGTG 12272

Qy   207 GlnThrTyrGlyAspAlaPheHisProArgProPheCysMetArgArgValLysGluMetAsp 226
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12273 CAGTACGGGTGACGCGCCTTCCACCCAAGGCCCTTCTGCATGCGGCCGCGTCAAGGAGATGGAC 12332

Qy   227 AlaTyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyr 246
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12333 GCCTATGGCATGGTCTCGCCCTTCGCCCGCCGGCCCTCAGCAGTGAACAGTGACCTCAAGTAC 12392

Qy   247 IleLysAlaLysValLeuArgGluGlyGlnAlaArgGluAspLysCysThrIleGln 266
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12393 ATCAAGGCCAAGGTCCTTCGGGAAGGCCAGGCCCGTGAGAGGGACAAGTGCACCATCCAG 12452

RESULT 13

US-10-723-860-458
; Sequence 458, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Ziotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 458
; LENGTH: 114771
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-458

Alignment Scores:

Pred. No.:		
Score:	911.00	
Percent Similarity:	98.33%	
Best Local Similarity:	97.78%	
Query Match:	66.16%	
DB:	18	

		Length:	114771
		Matches:	176
		Conservative:	1
		Mismatches:	3
		Indels:	0
		Gaps:	0

US-09-778-963B-2 (1-266) x US-10-723-860-458 (1-114771)

```
Qy    87 SerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgGluSerPhe  106
         ||||:|| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 57913 TCTCTCCCTGCAGGGGATNGTCTTCATCCTGGTTGTTCAGCCTGGATAACCGGGAGTCCTTC 57972

Qy   107 AspGluValLysArgLeuGlnLysGlnIleIleLeuGluValLysSerCysLeuLysAsnLys 126
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 57973 GATGAGGTCAAGCGCCTTCAGAAGCAGATAATCCTGGAGGTCAAGTCCTGCCTGAAGAACAAG 58032

Qy   127 ThrLysGluAlaAlaGluLeuProMetValIleCysGlyAsnLysAlaAspHisGlyGlu 146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 58033 ACCAAGGAGGCGGCGGAGCTGCCCATGGTCATCTGTGGCAACAAGGCAGACCACGGCGAG 58092

Qy   147 LeuCysArgGlnValProThrThrGluLeuLeuValSerGlyAspGluAsnSer 166
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 58093 CTGTGCCGGCAGGTGCCCACACCAGAGCTGCTGGTGTCGGGCGACGAGAACTGC 58152

Qy   167 AlaTyrPheGluValSerAlaLysAlaGlyAsnThrAsnValAspGluGluPheTyrValLeu 186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 58153 GCCTACTTCGAGGTGTCGGCCAAGAAGAACACCAACGTGGACGAGGAGTTCTACGTGCTC 58212

Qy   187 PheSerMetAlaLysSerLeuProHisGluMetSerProAlaLeuHisArgLysIleSerVal 206
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 58153 TTCAGCATGGCCAAGTCGCTGCCACACGAGATGAGCCCCGCCCTGCATCGCAAGATCTCCGTG 58272

Qy   207 GlnThrGlyAspAlaPheHisProArgProPheCysMetArgArgValLysGluMetAsp 226
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 58213 CAGACGGGTGACGCCTTCCACCCAGGCCCTTCTGCATGGCCCGGTCAAGGAGATGGAC 58272

Qy   227 AlaTyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyr 246
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 58273 GCCTATGGCATGGTCTCGCCCTTCGCCCGCCGTCAACAGTGACCTCAAGTAC 58332

Qy   247 IleLysAlaLysValLeuArgGluGlyLysGlnAlaArgGlyAspAspLysCysThrIleGln 266
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 58333 ATCAAGGCCAAGGTCCTTCGGGAAGGCCCAGGGCCCGTGAGAGGGACAAAGTGCACCATCCAG 58392
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RESULT 14
US-10-029-386-20951

; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;
; SEQ ID NO 20951
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022334.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EST HUMAN HIT: BI754083.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P10301, EVALUE 4.00e-10
; OTHER INFORMATION: NT HIT: gi16168170, EVALUE 0.000+00
US-10-029-386-20951

Alignment Scores:

Pred. No.:		
Score:	902.00	
Percent Similarity:	99.43%	
Best Local Similarity:	99.43%	
Query Match:	65.50%	
DB:	16	

		Length:	696
		Matches:	174
		Conservative:	0
		Mismatches:	1
		Indels:	0
		Gaps:	0

US-09-778-963B-2 (1-266) x US-10-029-386-20951 (1-696)

```
Qy    92 AspValPheIleLeuValPheSerLeuAspAsnArgGluSerPheAspGluValLysArg 111
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3 GATGTCTTCATCCTGGTTGTTCAGCCTGGATAACCGGGAGTCCTTCGATGAGGTCAAGCGC 62

Qy   112 LeuGlnLysGlnIleIleLeuGluValLysSerCysLeuLysAsnLysThrLysGluAlaAla 131
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    63 CTTCAGAAGCAGATAATCCTGGAGGTCAAGTCCTGCCTGAAGAACAAGACCAAGGAGGCGGCG 122

Qy   132 GluLeuProMetValIleCysGlyAsnLysAlaAspHisGlyGluLeuCysArgGlnVal 151
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 GAGCTGCCCATGGTCATCTGTGGCAACAAGGCAGACCACGGCGAGCTGTGCCGGCAGGTG 182

Qy   152 ProThrThrGluLeuLeuValSerGlyAspGluAsnSerAlaTyrPheGluVal 171
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   183 CCCACCACCGAGCTGCTGGTGTCGGGCGACGAGAACTGCGCCTACTTCGAGGTG 242

Qy   172 SerAlaLysAlaGlyAsnThrAsnValAspGluGluPheTyrValLeuPheSerMetAlaLys 191
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243 TCGGCCAAGAAGAACACCAACGTGGACGAGGAGTTCTACGTGCTCTTCAGCATGGCCAAG 302

Qy   192 SerLeuProHisGluMetSerProAlaLeuHisArgLysIleSerValGlnThrGlyAspAla 211
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 TCGCTGCCACACGAGATGAGCCCCGCCCTGCATCGCAAGATCTCCGTGCAGACGGGTGACGCC 362

Qy   212 PheHisProArgProPheCysMetArgArgValLysGluMetAspAlaTyrGlyMetVal 231
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 TTCCACCCCAGGCCCTTCTGCATGCGCCGGGTCAAGGAGATGGACGCCTATGGCATGGTC 422

Qy   232 SerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrIleLysAlaLysVal 251
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423 TCGCCCTTCGCCCGCCGCCCCAGCGTCAACAGTGACCTCAAGTACATCAAGGCCAAGGTC 482

Qy   252 LeuArgGluGlyLysGlnAlaArgGlyAspAspLysCysThrIleGln 266
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   483 CTTCGGGAAGGCCCAGGGCCCGTGAGAGGGACAAAGTGCACCATCCAG 527
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RESULT 15
US-10-804-491-1

; Sequence 1, Application US/10/804,491
; Publication No. US20040180375A1
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/804,491
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/09/709,103

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;  PRIOR FILING DATE: 2000-11-08
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: Patentin version 3.1
;
;  SEQ ID NO 1
;  LENGTH: 846
;  TYPE: DNA
;  ORGANISM: Homo Sapien
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(843)
;  OTHER INFORMATION:
US-10-804-491-1

Alignment Scores:
Pred. No.:
Score:                    3.97e-104
Percent Similarity:       879.00
Best Local Similarity:    77.70%
Query Match:              61.87%
DB:                       63.83%
                          18

                  Length:         846
                  Matches:        172
                  Conservative:   44
                  Mismatches:     46
                  Indels:         16
                  Gaps:           4

US-09-778-963B-2 (1-266) x US-10-804-491-1 (1-846)

Qy   1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr  20
         |||::|||  ||   :
Db  16 ATGATCAAGAAGAATGTCCCGACGGGACTCGGAGTATCCGGCCCAAGAACTCGTTAT    75

Qy  21 ArgMetValValLeuGlyValAlaSerArgValGlyLysSerSerIleValSerArgPheLeu  40
        |||||||||::|||||||||||
Db  76 CGGATGGTCATCCTCGGCCTCGTCCAAGGTGGGCAAGACGGCCCATCGTGTCCGCGCTTCCTC 135

Qy  41 AsnGlyValArgPheGluAspGlnThrTyrThrProThrIleGluAspPheHisArgLysValTyr  60
        ||::|||||||||||||
Db 136 ACCGGCGTCCGCTTCGAGACGCAGACCTACACGCCCACCATCGAAGACTTCCACCGAAGTTCTAC 195

Qy  61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe  80
        :::||||||||||||||||||||||||
Db 196 TCCATCCGCGGCGACATGTACCAGCTCGACATCCTCGACACCTCCGGCAACCACCCGTTC 255

Qy  81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
        |||||||||||||||||||||||
Db 256 CCCGCCATGCGCCGCCTCTCCATCCTCACAGGAGACGTTTTCATCCTGGTGTTCAGTCTG 315

Qy 101 AspAsnArgGluSerPheAspGluValValLysArgLeuGlnIleLeuGluValValLys 120
        |||::||||||||||||:::
Db 316 GACAACCGCGACTCTTTCGACGAGGTGCACCGGCCTCAGGCAGCAGATCCTCGACACCAAG 375

Qy 121 SerCysLeuLysLysAsnLysThrLysGluAlaAlaLeuAlaGluLeuProMetValIleLeuCysGlyAsn 140
        :::|||::|||||||||||
Db 376 TCTTGCCTCAAGAACAAAACCAAGGAGAACGCTGCACGTGGCCCCTGGTCATCTGCGGCAAC 435

Qy 141 LysAsnAspHisGlyLeuCysArgGlnValProThrThrGluAlaGluLeuLeuLeuVal 160
        |||||       :::
Db 436 AAGGGTGACCGC--GACTTCTACCCGGAGGTGGACCAGCCCGAGAATCGAGCAGCTGGTG 492

Qy 161 SerGlyAsp---GluAsnSerAlaTyrPheGluValSerArgAlaLysLysAsnThrAsnVal 179
        |||     :::
Db 493 GGCGACGACCCCCAGCGCTGCGCCTTACTTCGAGATCTCGGCAGAAGAACAGCAGCCTG 552

Qy 180 AspGluMetPheTyrValLeuPheSerMetAlaLysGluLeuProHisGluSerProAla 199
        :::||:|||||||
Db 553 GACCAGATGTTCCGGCGCCTTCGCCATGGCCAAGCTGCCCACGGAGGATGAGCCCAGAC 612

Qy 200 LeuHisIleArgGlyIleSerValGlnThrTyrGlyAspAlaPheHisProArgProCysMet 219
        |||||||||||||||||
Db 613 CTTGCACCGCAAGGTCTCGGTTGCAGTTACTGCGACGTTGCTGCACAAGAAG-----GCGCTG 666

Qy 220 ArgArgValLysGluMet------------AspAla 227
        |||||            :::
Db 667 CGGAACAAGAGAGCTCGTGGGCGCGGGCCGCAGAGGCGGCGGCGCCGACCCCGGCGGCC 726

Qy 228 TyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrIle 247
        :::|||::|||||||||||||||
Db 727 TTTGGCATCGTGGCACCCTTCGCGCGCGGCCGGCCCAGCGTACACAGCGGACCTCATGTACATC 786

Qy 248 LysAlaLysValLeuArgGluGlyGlnAlaArgGluArgAspLysCysThrIle 265
        :::||             |||
Db 787 CGCGAGAAGGCCAGCCCGCGGCCAGCGCCAAAGGACAAAGGAGGCTGCGTCATC 840
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Search completed: April 24, 2005, 07:51:00
Job time : 680 secs